

98	144.5	87.6	34	2	AAR55724	Parathorm
99	144.5	87.6	34	2	AAR58291	Lys(For)
100	144.5	87.6	34	2	AAR58017	Lys(N-ep

ALIGNMENTS

RESULT 1	
AAB91090	
ID	AAB91090 standard; peptide; 32 AA.
XX	
XX	
XX	AAB91090;
XX	
XX	
DT	22-JUN-2001 (first entry)
XX	
XX	
DE	Parathyroid hormone (PTH) related peptide SEQ ID NO:264.
XX	
KW	Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW	blood component; modification; succinimidyl; maleimido group; amino;
KW	hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS	Homc sapiens.
OS	Synthetic.
XX	
XX	WO200069900-A2.
XX	
XX	23-NOV-2000.
XX	
XX	17-MAY-2000; 2000WO-US013576.
XX	
XX	17-MAY-1999; 99US-0134406P.
PR	10-SEP-1999; 99US-0133406P.
PR	15-OCT-1999; 99US-0159783P.
XX	
XX	(CONJ-) CONJUCHEM INC.
PA	
XX	
XX	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI	
XX	
XX	WPI; 2001-117059/12.
DR	
XX	
XX	Modifying and attaching therapeutic peptides to albumin prevents
PT	peptidase degradation, useful for increasing length of in vivo activity.
PT	
XX	
PS	Disclosure; Page 278; 733pp; English.

The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity *in vivo* for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention

Q Sequence 32 AA; Query Match 90.6%; Score 149.5; DB 4; Length 32; Best Local Similarity 90.9%; Pred. NO. 1.5e-13; Matches 30; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

	match	conservative	match
QY	1	SVSEIQHXNKGKHLNSXERVEWLRKQLQDVHNY	33
Db	1	SVSEIOLHNLGKHLNS-ERVEWLRKQLQDVHNY	32

RESULT 2
AAB91091
ID AAB91091 standard; peptide; 32 AA.
XX
XX AAB91091;
XX AC
XX XX
DT 22-JUN-2001 (first entry)
XX
XX Parathyroid hormone (PTH) related peptide SEQ ID NO:265.
DE

Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyI; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.

Homo sapiens.

Synthetic.

WO200069900-A2.

23-NOV-2000.

17-MAY-2000; 2000WO-US013576.

17-MAY-1999; 99US-0134406P.

10-SEP-1999; 99US-0153406P.

15-OCT-1999; 99US-0159783P.

(CONJ-) CONJUCHEM INC.

Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K; WPI; 2001-112059/12.

Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.

Disclosure; Page 278; 733pp; English.

The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyI and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention

```

SQ      Sequence 32 AA;
Query Match      90.6%; Score 149.5; DB 4; Length 32;
Best Local Similarity 90.9%; Pred. No. 1.5e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy      1 SVSIIQHNKGGKHLNSXRVFWLRKKLQDVHNY 33
        |||||
Db      1 SVSBIQLHNLGKHLNS-ERVFWLRKKLQDVHNY 32
        |||||

RESULT 3
ABJ10726
ID      ABJ10726 standard; peptide; 34 AA.
XX

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```

AC ABJ10726;
XX
XX 02-DEC-2002 . (first entry)
XX
XX Human parathyroid hormone analogue #22.
XX
XX Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW PTHrP; analogue; abnormal CNS function; pancreatic function;
KW mineral metabolism; male infertility; abnormal blood pressure;
KW hypothalamic disease.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 7
FT /label= OTHER
FT /note= "OTHER=cyclohexylalanine"
FT Misc-difference 8
FT /note= "D-form residue"
FT Modified-site 11
FT /label= OTHER
FT Modified-site 18
FT /label= Nle
FT Modified-site 34
FT /note= "C-terminal amide"
FT Misc-difference 34
FT /note= "wild-type Phe substituted by Tyr"
XX
XX WO9957139-A2.
XX
XX 11-NOV-1999.
XX
XX 03-MAY-1999; 99WO-US009521.
XX
XX 05-MAY-1998; 98US-00072956.
XX
XX (SCRC ) SOC CONSEILS RECH & APPL SCI.
XX
XX Chorev M, Dong ZX, Rosenblatt M;
XX WPI; 2000-038790/03.
XX
XX New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
PT infertility, abnormal blood pressure or hypothalamic disease.
XX
XX Claim 11; Page 38; 49pp; English.
XX
XX The present invention provides a number of parathyroid hormone (PTH) or
CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
CC receptor agonists or antagonists and can be used in the treatment of
CC disorders resulting from altered or excessive action of the PTH2
CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
CC divergence from normal mineral metabolism and homeostasis, male
CC infertility, abnormal blood pressure or a hypothalamic disease. The
CC present sequence is a peptide analogue of the invention
XX
XX Sequence 34 AA;
SQ
Query Match 90.6%; Score 149.5; DB 3; Length 34;
Best Local Similarity 91.2%; Pred. No. 1.6e-13;
Matches 31; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGHLNSXERVEWLKRLQDVHNY 33
||||| |||||||
DB 1 SVSEIQLAHNLGKHLNSXERVEWLKRLQDVHNY 34
||||| |||||||

RESULT 4
ABJ10725
ID ABJ10725 standard; peptide; 34 AA.
XX
XX AC ABJ10725;
XX
XX 02-DEC-2002 (first entry)
XX
XX Human parathyroid hormone analogue #21.
XX
XX

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XX
KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW PTHrP; analogue; abnormal CNS function; pancreatic function;
KW mineral metabolism; male infertility; abnormal blood pressure;
KW hypothalamic disease.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 7
FT /label= OTHER
FT /note= "OTHER=cyclohexylalanine"
FT Misc-difference 8
FT /note= "D-form residue"
FT Modified-site 11
FT /label= OTHER
FT Modified-site 18
FT /label= Nle
FT Modified-site 34
FT /note= "C-terminal amide"
FT Misc-difference 34
FT /note= "wild-type Phe substituted by Tyr"
XX
XX WO9957139-A2.
XX
XX 11-NOV-1999.
XX
XX 03-MAY-1999; 99WO-US009521.
XX
XX 05-MAY-1998; 98US-00072956.
XX
XX (SCRC ) SOC CONSEILS RECH & APPL SCI.
XX
XX Chorev M, Dong ZX, Rosenblatt M;
XX WPI; 2000-038790/03.
XX
XX New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
PT infertility, abnormal blood pressure or hypothalamic disease.
XX
XX Claim 11; Page 38; 49pp; English.
XX
XX The present invention provides a number of parathyroid hormone (PTH) or
CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
CC receptor agonists or antagonists and can be used in the treatment of
CC disorders resulting from altered or excessive action of the PTH2
CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
CC divergence from normal mineral metabolism and homeostasis, male
CC infertility, abnormal blood pressure or a hypothalamic disease. The
CC present sequence is a peptide analogue of the invention
XX
XX Sequence 34 AA;
SQ
Query Match 90.6%; Score 149.5; DB 3; Length 34;
Best Local Similarity 94.1%; Pred. No. 1.6e-13;
Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGHLNSXERVEWLKRLQDVHNY 33
||||| |||||||
DB 1 SVSEIQXAHNKGHLNSXERVEWLKRLQDVHNY 34
||||| |||||||

RESULT 5
AAR07925
ID AAR07925 standard; protein; 34 AA.
XX
XX AC AAR07925;
XX
XX 18-FEB-1991 (first entry)
XX
XX

```


XX	New cyclic analogues of parathyroid hormone - having di:sulphide or amide
PT	bond between residues 13 and 17 and/or between residues 26 and 30, useful
PT	for treating osteoporosis and bone fractures.
XX	
PS	Claim 4; Page; 23pp; English.
XX	
CC	AAW19997 is a cyclised peptide derived from the N-terminal sequence of
CC	human parathyroid hormone (PTH). The peptide is able to bind to PTH
CC	receptors and stimulate adenylate cyclase activity. Cyclised PTH peptides
CC	stimulate bone growth and thus are useful in the treatment of
CC	osteoporosis and bone fractures. Optionally they may be administered
CC	concurrently with antiresorptive therapy (e.g. bisphosphonate and
CC	calcitonin). N.B. sequence not given in the specification, created from
CC	known sequence of amino acids 1-34 of human PTH
XX	
SQ	Sequence 34 AA;
	Query Match 90.0%; Score 148.5; DB 2; Length 34;
	Best Local Similarity 94.1%; Pred. No. 2.2e-13;
	Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy	1 SVSEIQ-XHNKGKHLNSXERVWLKRLQDVHNY 33
Db	1 SVSEIQHLNKGKHLNSXERVWLKRLQDVHNY 34
RESULT 9	
AAW2009	
ID	AAW20009 standard; peptide; 34 AA.
XX	
AC	AAW20009;
XX	
DT	28-AUG-1997 (first entry)
XX	
DE	Cyclised [Nle 8,18, Tyr 34] human parathyroid hormone (1-34) amide.
XX	
KW	Parathyroid hormone; PTH; amino terminus; cyclic; analogue;
KW	adenylate cyclase activity; bone growth; osteoporosis; fracture;
KW	antiresorptive therapy.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Modified-site 8
FT	/label= Nle
FT	/note= "wild-type Met replaced by Nle"
FT	
FT	Misc-difference 13
FT	/note= "joined via amide bond to residue 17"
FT	
FT	Misc-difference 17
FT	/note= "joined via amide bond to residue 13"
FT	
FT	Modified-site 18
FT	/label= Nle
FT	/note= "wild-type Met replaced by Nle"
FT	
FT	Misc-difference 26
FT	/note= "joined via amide bond to residue 30"
FT	
FT	Misc-difference 30
FT	/note= "joined via amide bond to residue 26"
FT	
FT	Modified-site 34
FT	/label= substitution
FT	/note= "wild-type Phe replaced by amidated Lys"
XX	
PN	WO9640193-A1.
XX	
XX	
PD	19-DEC-1996.
XX	
PF	06-JUN-1996; 96WO-US009674.
XX	
PR	07-JUN-1995; 95US-00488105.
XX	
PA	(BETH-) BETH ISRAEL HOSPITAL ASSOC.
XX	
PI	Chorev M, Rosenblatt M;

XX Parathyroid hormone analogue peptide compounds - used for stimulating
PT bone growth, e.g. in treatment of bone fractures or osteoporosis.
XX
PS Claim 6; Page; 24pp; English.

The invention relates to peptides of formula (I) containing at least one Acc (i.e. 1-amino-1-(3-9C cycloalkenyl)-carboxylic acid) residue. (R1)2Al¹-Val¹-Al3¹-Glu¹-As¹-Gln¹-A7¹-As¹-His¹-Asn¹-Al1¹-Al2¹-Lys¹-His¹-Al5¹-A-16¹-Al17¹-A-18¹-Al19¹-Arg¹-A21¹-A22¹-A23¹-A24¹-Arg¹-Lys¹-A27¹-A28¹-A29¹-A30¹-A31¹-A32¹-A33¹-A34¹-R3 (I); where Al¹ = Ser, Ala or Asp; A3¹, Al7¹ = Ser, Thr or Aib; A5¹, A7¹, Al1¹ = Leu, Nle, Ile, Cha, beta-Nal, Trp, Pail, Acc, Phe or p-(X)-Phe; X = OH, halo or Me; A8¹ = Met, Nva, Leu, Val, Ile, Cha, Acc or Nle; A12¹ = Gly, Acc or Aib; A16¹ = Ser, Asn, Ala or Aib; A18¹ = Met, Nva, Leu, Val, Ile, Nle, Acc, Cha or Aib; A19¹ = Glu or Aib; A21¹ = Val, Acc, Cha or Met; A22¹ = Acc or Glu; A¹23¹ = Trp, Acc or Cha; A24¹, A28¹ = Leu, Acc or Cha; A27¹ = Lys, Aib, Leu, hArg, Gln, Acc or Cha; A29¹ = Glu, Acc or Aib; A30¹ = Asp or Lys; A31¹ = Val, Leu, Nle, Acc or Cha, or is deleted; A32¹ = His or is deleted; A33¹ = Asn or is deleted; A34¹ = Phe, Tyr, Amp or Aib, or is deleted; R1, R2 = H, 1-12C alkyl, 2-12C alkenyl, 7-20C phenylalkyl, 11-20C naphthylalkyl, 1-12C hydroxyalkyl, 2-12C hydroxyalkenyl, 7-20C hydroxyphenylalkyl or 11-20C hydroxy-naphthylalkyl; one of R1 and R2 may also = COE; E = 1-12C alkyl, 2-12C alkenyl, 7-20C phenylalkyl, 11-20C naphthylalkyl, 1-12C hydroxyalkyl, 2-12C hydroxyalkenyl, 7-20C hydroxyphenylalkyl or 11-20C hydroxy-naphthylalkyl; R3 = OH, NH2, 1-12C alkoxy or -NH-Y-CH2-Z; Y = 1-12C hydrocarbyl; Z = H, OH, COOH or CONH2. The peptides are variants of fragments of parathyroid hormone (PTH) or parathyroid hormone-related protein (PTHrP). They stimulate bone growth, and are useful in the treatment of diseases or disorders associated with bone growth deficiency, e.g. osteoporosis and bone fractures. They are optionally used in conjunction with anti-resorptive therapy, e.g. with bis-phosphonates or calcitonin. The present sequence represents a specifically claimed peptide. NB: This sequence is not shown explicitly in the patent but was generated using the sequence of human parathyroid hormone as shown in Entrez Locus Number AAA29146

SQ Sequence 34 AA;

Query Match	90.0%	Score 148.5;	DB 2;
Best Local Similarity	97.1%	Pred. No. 2.e-13;	Length 34;
Matches 33;	Conservative	0;	Mismatches 0;
			Indels 1; Gaps 1;

Qy	1 SVSEIQ-XHNXGKHLNSXERVEWLKKLQDVHNY 33
Db	1 SVSEIOXHNXGKHLNSXERVEWLKKLQDVHNY 34

RESULT 12
AAW48392
ID AAW48392 standard; peptide; 34 AA.

DT 07-JUL-1998 (first entry)

DE Human parathyroid hormone biologically active region.

Parathyroid hormone related protein; PTHrP; osteoporosis;
calcium homeostasis.

OS Homo sapiens.

XX	FH	Key	Location/Qualifiers

FT	Region	5	/note= "Determines signalling capability"
----	--------	---	---

FT	Region	23	/note= "Determines binding affinity"
FT			

XX PN WO9804591-A1.

XX
PD
05-FEB-1998

XX
PF
30-JUL-1997: 97WO-US013360.

XX PR

31-JUL-1996; 96US-0025471P.

(GARD//) GARDELLA T J.

(JUEP/) JUEPPNER H.

Gardella TJ, Jueppner H;

WPI; 1998-130622/12.

Parathyroid hormone-related peptide analogues with agonist activity - at PTH/PTHrP receptor and either agonist or antagonist activity at PTH-2 receptor, used e.g. for treatment of osteoporosis.

Disclosure; Fig 3; 48pp; English.

The present sequence represents the biologically active region of human parathyroid hormone (PTH). PTH is a major regulator of calcium homeostasis whose principal target cells occur in bone and kidney. Some of the renal and skeletal actions of PTH appear to be mimicked by PTH related protein (PTHrP) which are believed to interact with the PTH receptor in these tissues. The invention creates hybrids (AAW48394-48398) of the active regions of PTH and PTHrP (AAW48393) to determine the residues involved in ligand-specificity of the PTH-2 receptor. It was found that Ile 5 determined signalling capabilities while Trp 23 determined binding affinity. The invention shows that by changing these two residues in PTHrP to the corresponding residues in PTH, PTHrP peptide analogues are created which are claimed to be selective agonists or antagonists of the PTH-2 receptor (AAW48399 and AAW48400). The antagonistic PTHrP peptide analogues are claimed to be useful in treating diseases involving altered or excessive activation of PTH-2 receptors (by inhibiting activation) while agonistic PTHrP peptide analogues are claimed to be useful in treating osteoporosis (by activating both PTH and PTH-2 receptors). PTHrP analogues are also useful for studying biological roles of the PTH-2 receptor and to identify specific sites of ligand-receptor interaction.

Sequence 34 AA;

Query Match 90.0%; Score 148.5; DB 2; Length 34;

Best Local Similarity 88.2%; Pred. No. 2.2e-13; Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

1 SVSEIQ-XHNXGKHLNSXERVEWLRKKLQDVHNY 33

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLODVHNY 34

RESULT 13

ABJ10720

ID ABJ10720 standard; peptide; 34 AA.

AC ABJ10720;

AA
DT 02-DEC-2002 (first entry)XX
DE
Human parathyroid hormone analogue #16.

Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
 KW
 PTHrP; analogue; abnormal CNS function; pancreatic function;
 KW
 mineral metabolism; male infertility; abnormal blood pressure;
 KW
 hypothalamic disease.
 KW

XX
OS Homo sapiens.

OS Homo sapiens
OS Synthetic.
OS Synthetic.

XX	Key	Location/Qualifiers
FH		

FT Modified-site

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FT /label= OTHER
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Misc-difference 8

ET	Modified-site	/n
ET	Modified-site	11

FT	Modified-site	34	
FT	/notes= "C-terminal amide"		
FT	Misc-difference	34	
FT	/note= "wild-type Phe substituted by Tyr"		
XX			
XX	WO9957139-A2.		
XX			
XX	11-NOV-1999.		
XX			
XX	03-MAY-1999;	99WO-US009521.	
XX			
XX	05-MAY-1998;	98US-00072956.	
XX			
XX	(SCRC) SOC CONSEILS RECH & APPL SCI.		
XX			
XX	Chorev M, Dong ZX, Rosenblatt M;		
XX			
XX	WPI; 2000-038790/03.		
XX			
XX	New parathyroid hormone analogs, used for treating e.g. abnormal CNS or		
XX	pancreatic functions, abnormal mineral metabolism and homeostasis, male		
XX	infertility, abnormal blood pressure or hypothalamic disease.		
XX			
XX	Claim 11; Page 38; 49pp; English.		
XX			
XX	The present invention provides a number of parathyroid hormone (PTH) or		
XX	parathyroid hormone-related protein (PTHrP) analogues. These act as PTHrP		
XX	receptor agonists or antagonists and can be used in the treatment of		
XX	disorders resulting from altered or excessive action of the PTHrP		
XX	receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,		
XX	divergence from normal mineral metabolism and homeostasis, male		
XX	infertility, abnormal blood pressure or a hypothalamic disease. The		
XX	present sequence is a peptide analogue of the invention		
XX			
SQ	Sequence 34 AA;		
	Query Match	90.0%; Score 148.5; DB 3; Length 34;	
	Best Local Similarity	94.1%; Pred. No. 2.2e-13;	
	Matches	33; Conservative 0; Mismatches 1; Indels 1; Gaps	
Qy	1 SVSEIQ-XHNKXGHLNSXERVEWLKKLQDVHNY 33		
Db	1 SVSEIQXHNKXGHLNSXERVEWLKKLQDVHNY 34		
RESULT 16			
ABU10747			
ID	ABU10747 standard; peptide; 34 AA.		
XX			
AC	ABJ10747;		
XX			
DT	02-DEC-2002 (first entry)		
XX			
DE	Human parathyroid hormone analogue #43.		
XX			
KW	Human; parathyroid hormone; parathyroid hormone-related protein; PTH;		
KW	PTHrP; analogue; abnormal CNS function; pancreatic function;		
KW	mineral metabolism; male infertility; abnormal blood pressure;		
KW	hypothalamic disease.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	
FT	Modified-site	7	
FT	/label= OTHER		
FT	/note= "OTHER=des-Leu"		
FT	Modified-site	8	
FT	/label= Nle		
FT	Modified-site	18	
FT	/label= Nle		
FT	Modified-site	34	
FT	/note= "C-terminal amide"		

FT	Misc-difference	34
FT	/note= "wild-type Phe substituted by Tyr"	
XX		
PV	WO9957139-A2.	
PN		
XX	11-NOV-1999.	
PD		
XX		
XX	03-MAY-1999;	99WO-US009521.
XX		
PF		
XX	05-MAY-1998;	98US-00072956.
PR		
XX	(SCRC) SOC CONSEILS RECH & APPL SCI.	
XX		
PA	Chorev M, Dong ZX, Rosenblatt M;	
PI	WPI; 2000-038790/03.	
PP		
DR		
XX	New parathyroid hormone analogs, used for treating e.g. abnormal CNS or	
XX	pancreatic functions, abnormal mineral metabolism and homeostasis, male	
PT	infertility, abnormal blood pressure or hypothalamic disease.	
PT		
XX		
PS	Claim 11; Page 39; 49pp; English.	
PS		
XX	The present invention provides a number of parathyroid hormone (PTH) or	
CC	parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2	
CC	receptor agonists or antagonists and can be used in the treatment of	
CC	disorders resulting from altered or excessive action of the PTH2	
CC	receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,	
CC	divergence from normal mineral metabolism and homeostasis, male	
CC	infertility, abnormal blood pressure or a hypothalamic disease. The	
CC	present sequence is a peptide analogue of the invention	
XX		
SQ	Sequence 34 AA;	
	Query Match	90.0%; Score 148.5; DB 3; Length 34;
	Best Local Similarity	94.1%; Pred. No. 2.2e-13;
	Matches 32; Conservative	0; Mismatches 1; Indels 1; Gaps 1;
QY	1 SVSEIQ-XHNXGKHLNSXERVEWLRRKKLDQVHNY 33	
DB	1 SVSEIQXNINLGHLSXERVEWLRRKKLDQVHNY 34	
RESULT 17		
ABJ10750		
ID	ABJ10750 standard; peptide; 34 AA.	
XX		
AC	ABJ10750;	
XX		
DT	02-DEC-2002 (first entry)	
XX		
DE	Human parathyroid hormone analogue #46.	
XX		
KW	Human; parathyroid hormone; parathyroid hormone-related protein; PTH;	
KW	PTHrP; analogue; abnormal CNS function; pancreatic function;	
KW	mineral metabolism; male infertility; abnormal blood pressure;	
KW	hypothalamic disease.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	8 /label= Nle
FT		
FT	Modified-site	11 /label= OTHER
FT		
FT	Modified-site	18 /note= "des-Leu"
FT		
FT	Modified-site	19 /label= Nle
FT		
FT	Modified-site	34 /note= "C-terminal amide"
FT		
FT	Misc-difference	34 /note= "wild-type Phe substituted by Tyr"
FT		

XX WO9957139-A2.
XX 11-NOV-1999.
XX 03-MAY-1999; 99WO-US009521.
XX 05-MAY-1998; 98US-00072956.
XX (SCRC) SOC CONSEILS RECH & APPL SCI.
XX Chorev M, Dong ZX, Rosenblatt M;
XX WPI; 2000-038790/03.
XX New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
XX pancreatic functions, abnormal mineral metabolism and homeostasis, male
XX infertility, abnormal blood pressure or hypothalamic disease.
XX Claim 11; Page 39; 49pp; English.
XX The present invention provides a number of parathyroid hormone (PTH) or
XX parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
XX receptor agonists or antagonists and can be used in the treatment of
XX disorders resulting from altered or excessive action of the PTH2
XX receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
XX divergence from normal mineral metabolism and homeostasis, male
XX infertility, abnormal blood pressure or a hypothalamic disease. The
XX present sequence is a peptide analogue of the invention
XX Sequence 34 AA;
Query Match 90.0%; Score 148.5; DB 3; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.2e-13;
Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
DB 1 SVSEIQLXHNXGKHLNSXERVELRKKLQDVHNY 34
RESULT 18
ABJ10715
ID ABJ10715 standard; peptide; 34 AA.
XX AC ABJ10715;
XX DT 02-DEC-2002 (first entry)
XX DE Human parathyroid hormone analogue #11.
XX Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
XX PTHrP; analogue; abnormal CNS function; pancreatic function;
XX mineral metabolism; male infertility; abnormal blood pressure;
XX hypothalamic disease.
XX Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 7 /label= OTHER
XX FT /note= "OTHER=cyclohexylalanine"
XX FT Misc-difference 8 /note= "D-form residue"
XX FT Modified-site 11 /label= OTHER
XX FT /note= "OTHER=cyclohexylalanine"
XX FT Modified-site 18 /label= Nle
XX FT Modified-site 34 /note= "C-terminal amide"
XX FT Misc-difference 34

FT XX /note= "wild-type Phe substituted by Tyr"
XX WO9957139-A2.
XX 11-NOV-1999.
XX 03-MAY-1999; 99WO-US009521.
XX 05-MAY-1998; 98US-00072956.
XX (SCRC) SOC CONSEILS RECH & APPL SCI.
XX Chorev M, Dong ZX, Rosenblatt M;
XX WPI; 2000-038790/03.
XX New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
XX pancreatic functions, abnormal mineral metabolism and homeostasis, male
XX infertility, abnormal blood pressure or hypothalamic disease.
XX Claim 11; Page 38; 49pp; English.
XX The present invention provides a number of parathyroid hormone (PTH) or
XX parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
XX receptor agonists or antagonists and can be used in the treatment of
XX disorders resulting from altered or excessive action of the PTH2
XX receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
XX divergence from normal mineral metabolism and homeostasis, male
XX infertility, abnormal blood pressure or a hypothalamic disease. The
XX present sequence is a peptide analogue of the invention
XX Sequence 34 AA;
Query Match 90.0%; Score 148.5; DB 3; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.2e-13;
Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
DB 1 SVSEIQIXHNXGKHLNSXERVELRKKLQDVHNY 34
RESULT 19
ABJ10734
ID ABJ10734 standard; peptide; 34 AA.
XX AC ABJ10734;
XX DT 02-DEC-2002 (first entry)
XX DE Human parathyroid hormone analogue #30.
XX Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
XX PTHrP; analogue; abnormal CNS function; pancreatic function;
XX mineral metabolism; male infertility; abnormal blood pressure;
XX hypothalamic disease.
XX Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 7 /label= OTHER
XX FT /note= "OTHER=cyclohexylalanine"
XX FT Modified-site 8 /label= Abu
XX FT /note= "D-form residue"
XX FT Modified-site 11 /label= OTHER
XX FT /note= "OTHER=cyclohexylalanine"
XX FT Modified-site 18 /label= Nle
XX FT Modified-site 34

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FT Misc-difference 34 /note= "C-terminal amide"
FT FT /note= "wild-type Phe substituted by Tyr"
PN XX
PD XX
XX WO9957139-A2.
XX 11-NOV-1999.
XX 03-MAY-1999; 99WO-US009521.
XX 05-MAY-1998; 98US-00072956.
XX (SCRC ) SOC CONSEILS RECH & APPL SCI.
XX Choev M, Dong ZX, Rosenblatt M;
XX WPI; 2000-038790/03.
XX New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
XX pancreatic functions, abnormal mineral metabolism and homeostasis, male
XX infertility, abnormal blood pressure or hypothalamic disease.
XX Claim 11; Page 38; 49pp; English.
XX The present invention provides a number of parathyroid hormone (PTH) or
XX parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
XX receptor agonists or antagonists and can be used in the treatment of
XX disorders resulting from altered or excessive action of the PTH2
XX receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
XX divergence from normal mineral metabolism and homeostasis, male
XX infertility, abnormal blood pressure or a hypothalamic disease. The
XX present sequence is a peptide analogue of the invention
XX Sequence 34 AA;
XX Query Match 90.0%; Score 148.5; DB 3; Length 34;
XX Best Local Similarity 97.1%; Pred. No. 2.2e-13;
XX Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 1 SVSEIQXHNXGKHLNSXERVELRKKLQDVHNY 34
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX RESULT 20
XX ABJ10745
XX ID ABJ10745 standard; peptide; 34 AA.
XX AC ABJ10745;
XX 02-DEC-2002 (first entry)
XX Human parathyroid hormone analogue #41.
XX Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
XX PTHrP; analogue; abnormal CNS function; pancreatic function;
XX mineral metabolism; male infertility; abnormal blood pressure;
XX hypothalamic disease.
XX Homo sapiens.
XX OS Synthetic.
XX Key Location/Qualifiers
XX FT Misc-difference 8 /label= Nle
XX FT Modified-site 34 /note= "norleucine, D-form residue"
XX FT Modified-site 18 /label= OTHER
XX FT Modified-site 34 /note= "OTHER-des-Met"
XX FT Modified-site 34 /note= "C-terminal amide"
XX FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"
XX FT
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XX WO9957139-A2.
XX 11-NOV-1999.
XX 03-MAY-1999; 99WO-US009521.
XX 05-MAY-1998; 98US-00072956.
XX (SCRC ) SOC CONSEILS RECH & APPL SCI.
XX Choev M, Dong ZX, Rosenblatt M;
XX WPI; 2000-038790/03.
XX New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
XX pancreatic functions, abnormal mineral metabolism and homeostasis, male
XX infertility, abnormal blood pressure or hypothalamic disease.
XX Claim 11; Page 39; 49pp; English.
XX The present invention provides a number of parathyroid hormone (PTH) or
XX parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
XX receptor agonists or antagonists and can be used in the treatment of
XX disorders resulting from altered or excessive action of the PTH2
XX receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
XX divergence from normal mineral metabolism and homeostasis, male
XX infertility, abnormal blood pressure or a hypothalamic disease. The
XX present sequence is a peptide analogue of the invention
XX Sequence 34 AA;
XX Query Match 90.0%; Score 148.5; DB 3; Length 34;
XX Best Local Similarity 94.1%; Pred. No. 2.2e-13;
XX Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 1 SVSEIQLXHNLGKHLNSXERVELRKKLQDVHNY 34
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX RESULT 21
XX ABJ10772
XX ID ABJ10772 standard; peptide; 34 AA.
XX AC ABJ10772;
XX 02-DEC-2002 (first entry)
XX Human parathyroid hormone analogue #68.
XX Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
XX PTHrP; analogue; abnormal CNS function; pancreatic function;
XX mineral metabolism; male infertility; abnormal blood pressure;
XX hypothalamic disease.
XX Homo sapiens.
XX OS Synthetic.
XX Key Location/Qualifiers
XX FT Misc-difference 8 /note= "D-form residue"
XX FT Modified-site 34 /note= "C-terminal amide"
XX FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"
XX FT
XX WO9957139-A2.
XX 11-NOV-1999.
XX 03-MAY-1999; 99WO-US009521.
XX
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XX PF 03-MAY-1999; 99WO-US009521.
 XX XX
 XX PR 05-MAY-1998; 98US-00072956.
 XX XX
 XX PA (SCRC) SOC CONSEILS RECH & APPL SCI.
 XX PI Chorev M, Dong ZX, Rosenblatt M;
 XX DR WPI; 2000-038790/03.
 XX XX
 XX PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
 PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
 PT infertility, abnormal blood pressure or hypothalamic disease.
 XX PS Claim 11; Page 39; 49pp; English.
 XX CC The present invention provides a number of parathyroid hormone (PTH) or
 CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
 CC receptor agonists or antagonists and can be used in the treatment of
 CC disorders resulting from altered or excessive action of the PTH2
 CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
 CC divergence from normal mineral metabolism and homeostasis, male
 CC infertility, abnormal blood pressure or a hypothalamic disease. The
 CC present sequence is a peptide analogue of the invention
 XX SQ Sequence 34 AA;
 Query Match 90.0%; Score 148.5; DB 3; Length 34;
 Best Local Similarity 94.1%; Pred. No. 2.2e-13;
 Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 SVSEIQ-XHNKXGKHLNSXERVEWLKKLQDVHNY 33
 DB 1 SVSEIQXHNKXGKHLNSXERVEWLKKLQDVHNY 34
 RESULT 24
 ABJ10709
 ID ABJ10709 standard; peptide; 34 AA.
 XX AC ABJ10709;
 XX DT 02-DEC-2002 (first entry)
 XX DE Human parathyroid hormone analogue #5.
 XX KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
 KW PTHrP; analogue; abnormal CNS function; pancreatic function;
 KW mineral metabolism; male infertility; abnormal blood pressure;
 KW hypothalamic disease.
 XX OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 8
 FT Misc-difference /note= "D-form residue"
 FT Modified-site 18
 FT /label= Nle
 FT Modified-site 34
 FT /note= "norleucine"
 FT Misc-difference 34
 FT /note= "C-terminal amide"
 FT /note= "wild-type Phe substituted by Tyr"
 XX PN WO9957139-A2.
 XX PD 11-NOV-1999.
 XX PF 03-MAY-1999; 99WO-US009521.
 XX PR 05-MAY-1998; 98US-00072956.

XX PA (SCRC) SOC CONSEILS RECH & APPL SCI.
 XX XX
 XX PI Chorev M, Dong ZX, Rosenblatt M;
 XX XX
 XX DR WPI; 2000-038790/03.
 XX XX
 XX PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
 PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
 PT infertility, abnormal blood pressure or hypothalamic disease.
 XX PS Claim 11; Page 38; 49pp; English.
 XX CC The present invention provides a number of parathyroid hormone (PTH) or
 CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
 CC receptor agonists or antagonists and can be used in the treatment of
 CC disorders resulting from altered or excessive action of the PTH2
 CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
 CC divergence from normal mineral metabolism and homeostasis, male
 CC infertility, abnormal blood pressure or a hypothalamic disease. The
 CC present sequence is a peptide analogue of the invention
 XX SQ Sequence 34 AA;
 Query Match 90.0%; Score 148.5; DB 3; Length 34;
 Best Local Similarity 91.2%; Pred. No. 2.2e-13;
 Matches 31; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 1 SVSEIQ-XHNKXGKHLNSXERVEWLKKLQDVHNY 33
 DB 1 SVSEIQLEHNLGKHLNSXERVEWLKKLQDVHNY 34
 RESULT 25
 ABJ10741
 ID ABJ10741 standard; peptide; 34 AA.
 XX AC ABJ10741;
 XX DT 02-DEC-2002 (first entry)
 XX DE Human parathyroid hormone analogue #37.
 XX KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
 KW PTHrP; analogue; abnormal CNS function; pancreatic function;
 KW mineral metabolism; male infertility; abnormal blood pressure;
 KW hypothalamic disease.
 XX OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 8
 FT /label= OTHER
 FT /note= "OTHER-des-Met"
 FT Modified-site 18
 FT /label= Nle
 FT Modified-site 34
 FT /note= "C-terminal amide"
 FT Misc-difference 34
 FT /note= "wild-type Phe substituted by Tyr"
 XX PN WO9957139-A2.
 XX PD 11-NOV-1999.
 XX PF 03-MAY-1999; 99WO-US009521.
 XX PR 05-MAY-1998; 98US-00072956.
 XX PA (SCRC) SOC CONSEILS RECH & APPL SCI.
 XX PI Chorev M, Dong ZX, Rosenblatt M;

XX WPI; 2000-038790/03.
XX New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
XX pancreatic functions, abnormal mineral metabolism and homeostasis, male
PT infertility, abnormal blood pressure or hypothalamic disease.
PT
XX Claim 11; Page 39; 49pp; English.
XX
CC The present invention provides a number of parathyroid hormone (PTH) or
CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
CC receptor agonists or antagonists and can be used in the treatment of
CC disorders resulting from altered or excessive action of the PTH2
CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
CC divergence from normal mineral metabolism and homeostasis, male
CC infertility, abnormal blood pressure or a hypothalamic disease. The
CC present sequence is a peptide analogue of the invention
XX
SQ Sequence 34 AA;
Query Match 90.0%; Score 148.5; DB 3; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.2e-13;
Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 SVSEIQ-XHNXGKHLNSXERVEWLRKKLQDVHNY 33
Db 1 SVSEIQLXHNLGKHLNSXERVEWLRKKLQDVHNY 34
RESULT 26
ABJ10732
ID ABJ10732 standard; peptide; 34 AA.
AC ABJ10732;
XX
XX 02-DEC-2002 (first entry)
XX Human parathyroid hormone analogue #28.
XX
XX Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW PTHrP; analogue; abnormal CNS function; pancreatic function;
KW mineral metabolism; male infertility; abnormal blood pressure;
KW hypothalamic disease.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 8 /note= "D-form residue"
FT Modified-site 18 /label= Nle
FT Modified-site 34 /note= "C-terminal amide"
FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"
XX
XX WO9957139-A2.
XX
XX 11-NOV-1999.
XX
XX 03-MAY-1999; 99WO-US009521.
XX
XX 05-MAY-1998; 98US-00072956.
XX (SCRC) SOC CONSEILS RECH & APPL SCI.
XX
XX Choev M, Dong ZX, Rosenblatt M;
XX WPI; 2000-038790/03.
XX
XX New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
XX pancreatic functions, abnormal mineral metabolism and homeostasis, male

PT infertility, abnormal blood pressure or hypothalamic disease.
XX
XX Claim 11; Page 38; 49pp; English.
XX
CC The present invention provides a number of parathyroid hormone (PTH) or
CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
CC receptor agonists or antagonists and can be used in the treatment of
CC disorders resulting from altered or excessive action of the PTH2
CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
CC divergence from normal mineral metabolism and homeostasis, male
CC infertility, abnormal blood pressure or a hypothalamic disease. The
CC present sequence is a peptide analogue of the invention
XX
SQ Sequence 34 AA;
Query Match 90.0%; Score 148.5; DB 3; Length 34;
Best Local Similarity 91.2%; Pred. No. 2.2e-13;
Matches 31; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 SVSEIQ-XHNXGKHLNSXERVEWLRKKLQDVHNY 33
Db 1 SVSEIQLWHNLGKHLNSXERVEWLRKKLQDVHNY 34
RESULT 27
ABJ10708
ID ABJ10708 standard; peptide; 34 AA.
XX
XX AC ABJ10708;
XX
XX 02-DEC-2002 (first entry)
XX Human parathyroid hormone analogue #4.
XX
XX Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW PTHrP; analogue; abnormal CNS function; pancreatic function;
KW mineral metabolism; male infertility; abnormal blood pressure;
KW hypothalamic disease.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 8 /label= OTHER
FT Modified-site 18 /note= "OTHER=cyclohexylalanine, D-form residue"
FT Modified-site 18 /label= Nle
FT Modified-site 34 /note= "C-terminal amide"
FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"
XX
XX WO9957139-A2.
XX
XX 11-NOV-1999.
XX
XX 03-MAY-1999; 99WO-US009521.
XX
XX 05-MAY-1998; 98US-00072956.
XX (SCRC) SOC CONSEILS RECH & APPL SCI.
XX
XX Choev M, Dong ZX, Rosenblatt M;
XX WPI; 2000-038790/03.
XX
XX New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
XX pancreatic functions, abnormal mineral metabolism and homeostasis, male
XX infertility, abnormal blood pressure or hypothalamic disease.
XX
XX Claim 11; Page 38; 49pp; English.
XX

CC The present invention provides a number of parathyroid hormone (PTH) or
CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
CC receptor agonists or antagonists and can be used in the treatment of
CC disorders resulting from altered or excessive action of the PTH2
CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
CC divergence from normal mineral metabolism and homeostasis, male
CC infertility, abnormal blood pressure or a hypothalamic disease. The
CC present sequence is a peptide analogue of the invention
XX Sequence 34 AA;
SQ

Query Match 90.0%; Score 148.5; DB 3; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.2e-13;
Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
Db 1 SVSEIQXHNXGKHLNSXERVELRKKLQDVHNY 34

RESULT 28
ABJ10711
ID ABJ10711 standard; peptide; 34 AA.
XX
XX ABJ10711;
XX
DT 02-DEC-2002 (first entry)
XX
DE Human parathyroid hormone analogue #7.
XX
KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW PTHrP; analogue; abnormal CNS function; pancreatic function;
KW mineral metabolism; male infertility; abnormal blood pressure;
KW hypothalamic disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 8 /label= Abu
FT /note= "D-form residue"
FT
FT Modified-site 18 /label= Nle
FT /label= Nle
FT Modified-site 34 /note= "C-terminal amide"
FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"
FT
XX WO9957139-A2.
XX
XX PD 11-NOV-1999.
XX
XX PF 03-MAY-1999; 99WO-US009521.
XX
XX PR 05-MAY-1998; 98US-00072956.
XX
XX PA (SCRC) SOC CONSEILS RECH & APPL SCI.
XX
XX PI Chorev M, Dong ZX, Rosenblatt M;
XX WPI; 2000-038790/03.
XX
XX DR New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
XX pancreatic functions, abnormal mineral metabolism and homeostasis, male
XX infertility, abnormal blood pressure or hypothalamic disease.
XX Claim 11; Page 38; 49pp; English.
XX
XX PS The present invention provides a number of parathyroid hormone (PTH) or
XX parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
XX receptor agonists or antagonists and can be used in the treatment of
XX disorders resulting from altered or excessive action of the PTH2

CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
CC divergence from normal mineral metabolism and homeostasis, male
CC infertility, abnormal blood pressure or a hypothalamic disease. The
CC present sequence is a peptide analogue of the invention
XX Sequence 34 AA;
SQ

Query Match 90.0%; Score 148.5; DB 3; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.2e-13;
Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
Db 1 SVSEIQXHNXGKHLNSXERVELRKKLQDVHNY 34

RESULT 29
ABJ10731
ID ABJ10731 standard; peptide; 34 AA.
XX
XX ABJ10731;
XX
DT 02-DEC-2002 (first entry)
XX
DE Human parathyroid hormone analogue #27.
XX
KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW PTHrP; analogue; abnormal CNS function; pancreatic function;
KW mineral metabolism; male infertility; abnormal blood pressure;
KW hypothalamic disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /label= OTHER
FT /note= "OTHER=cyclohexylalanine"
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 11 /label= OTHER
FT /label= OTHER
FT Modified-site 18 /note= "OTHER=cyclohexylalanine"
FT /label= Nle
FT Modified-site 34 /note= "C-terminal amide"
FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"
FT
XX WO9957139-A2.
XX
XX PD 11-NOV-1999.
XX
XX PF 03-MAY-1999; 99WO-US009521.
XX
XX PR 05-MAY-1998; 98US-00072956.
XX
XX PA (SCRC) SOC CONSEILS RECH & APPL SCI.
XX
XX PI Chorev M, Dong ZX, Rosenblatt M;
XX WPI; 2000-038790/03.
XX
XX DR New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
XX pancreatic functions, abnormal mineral metabolism and homeostasis, male
XX infertility, abnormal blood pressure or hypothalamic disease.
XX Claim 11; Page 38; 49pp; English.
XX
XX PS The present invention provides a number of parathyroid hormone (PTH) or
XX parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
XX receptor agonists or antagonists and can be used in the treatment of

CC disorders resulting from altered or excessive action of the PTH2
 CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
 CC divergence from normal mineral metabolism and homeostasis, male
 CC infertility, abnormal blood pressure or a hypothalamic disease. The
 CC present sequence is a peptide analogue of the invention
 XX SQ Sequence 34 AA;
 Query Match 90.0%; Score 148.5; DB 3; Length 34;
 Best Local Similarity 97.1%; Pred. No. 2.2e-13;
 Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 SVSEIQX-HNXGKHLNSXERVEWLKRLQDVHNY 33
 DB 1 SVSEIQXHNXGKHLNSXERVEWLKRLQDVHNY 34
 RESULT 30
 ABJ10705
 ID ABJ10705 standard; peptide; 34 AA.
 XX AC ABJ10705;
 XX DT 02-DEC-2002 (first entry)
 XX DE Human parathyroid hormone analogue #1.
 XX KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
 KW PTHrP; analogue; abnormal CNS function; pancreatic function;
 KW mineral metabolism; male infertility; abnormal blood pressure;
 KW hypothalamic disease.
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 8 /label= Nle
 FT /note= "norleucine, D-form residue"
 FT Modified-site 18 /label= Nle
 FT Modified-site 34 /note= "C-terminal amide"
 FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"
 XX PN W0957139-A2.
 XX PD 11-NOV-1999.
 XX PF 03-MAY-1999; 99WO-US009521.
 XX PR 05-MAY-1998; 98US-00072956.
 XX PA (SCRC) SOC CONSEILS RECH & APPL SCI.
 XX PI Chorev M, Dong ZX, Rosenblatt M;
 XX DR WPI; 2000-038790/03.
 XX PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
 PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
 PT infertility, abnormal blood pressure or hypothalamic disease.
 XX PS Claim 11; Page 38; 49pp; English.
 XX CC The present invention provides a number of parathyroid hormone (PTH) or
 CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
 CC receptor agonists or antagonists and can be used in the treatment of
 CC disorders resulting from altered or excessive action of the PTH2
 CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
 CC divergence from normal mineral metabolism and homeostasis, male
 CC infertility, abnormal blood pressure or a hypothalamic disease. The

CC present sequence is a peptide analogue of the invention
 XX SQ Sequence 34 AA;
 Query Match 90.0%; Score 148.5; DB 3; Length 34;
 Best Local Similarity 94.1%; Pred. No. 2.2e-13;
 Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 SVSEIQX-HNXGKHLNSXERVEWLKRLQDVHNY 33
 DB 1 SVSEIQLXHNXGKHLNSXERVEWLKRLQDVHNY 34
 RESULT 31
 ABJ10768
 ID ABJ10768 standard; peptide; 34 AA.
 XX AC ABJ10768;
 XX DT 02-DEC-2002 (first entry)
 XX DE Human parathyroid hormone analogue #64.
 XX KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
 KW PTHrP; analogue; abnormal CNS function; pancreatic function;
 KW mineral metabolism; male infertility; abnormal blood pressure;
 KW hypothalamic disease.
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 7 /label= OTHER
 FT /note= "OTHER=cyclohexylalanine"
 FT Modified-site 8 /label= Nle
 FT /note= "D-form residue"
 FT Modified-site 11 /label= OTHER
 FT /note= "OTHER=cyclohexylalanine"
 FT Modified-site 18 /label= OTHER
 FT /note= "OTHER=des-Met"
 FT Modified-site 34 /note= "C-terminal amide"
 FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"
 XX PN W0957139-A2.
 XX PD 11-NOV-1999.
 XX PF 03-MAY-1999; 99WO-US009521.
 XX PR 05-MAY-1998; 98US-00072956.
 XX PA (SCRC) SOC CONSEILS RECH & APPL SCI.
 XX PI Chorev M, Dong ZX, Rosenblatt M;
 XX DR WPI; 2000-038790/03.
 XX PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
 PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
 PT infertility, abnormal blood pressure or hypothalamic disease.
 XX PS Claim 11; Page 39; 49pp; English.
 XX CC The present invention provides a number of parathyroid hormone (PTH) or
 CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
 CC receptor agonists or antagonists and can be used in the treatment of
 CC disorders resulting from altered or excessive action of the PTH2

parathyroid hormone-related protein (PTHrP) analogues. These act as PTHrP receptor agonists or antagonists and can be used in the treatment of disorders resulting from altered or excessive action of the PTHrP receptor, e.g. abnormal CNS functions, abnormal pancreatic functions, divergence from normal mineral metabolism and homeostasis, male infertility, abnormal blood pressure or a hypothalamic disease. The present sequence is a peptide analogue of the invention

Query Match 90.0%; Score 148.5; DB 3; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.2e-13;
Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNXGHLNSXERVEWLKKLQDVHNY 33
|||||

Dp 1 SVSEIOFHNGKHLNSXERVEWLKKLQDVHNY 34
|||||

RESULT 34	
ABJ10723	
ID	ABJ10723 standard; peptide; 34 AA.
XX	
XX	
AC	ABJ10723;
XX	
DT	02-DEC-2002 (first entry)
XX	
XX	
DE	Human parathyroid hormone analogue #19.
XX	
XX	
KW	Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW	PTHrP; analogue; abnormal CNS function; pancreatic function;
KW	mineral metabolism; male infertility; abnormal blood pressure;
KW	hypothalamic disease.

Key	Location/Qualifiers
Modified-site	7
FT	/label= OTHER
FT	/note= "OTHER=cyclohexylalanine"
FT	8
Modified-site	/label= OTHER
FT	/note= "OTHER=cyclohexylalanine, D-form residue"
FT	11
Modified-site	/label= OTHER
FT	/note= "OTHER=cyclohexylalanine"
FT	18
Modified-site	/label= Nle
FT	34
Modified-site	/note= "C-terminal amide"
FT	34
Misc-difference	/note= "wild-type phe substituted by Tyr"
FT	
FT	

XX	WO9957139-A2.
XX	
XX	
PD	11-NOV-1999.
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PF	03-MAY-1999; 99WO-US009521.
XX	
XX	
PR	05-MAY-1998; 98US-00072956.
XX	
XX	
PA	(SCRC) SOC CONSEILS RECH & APPL SCI.
XX	
PI	Chorev M, Dong ZX, Rosenblatt M;
XX	
DR	WPI; 2000-038790/03.

xx CC The present invention provides a number of parathyroid hormone (PTH) or
CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
CC receptor agonists or antagonists and can be used in the treatment of
CC disorders resulting from altered or excessive action of the PTH2
CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
CC divergence from normal mineral metabolism and homeostasis, male
CC infertility, abnormal blood pressure or a hypothalamic disease. The
CC present sequence is a peptide analogue of the invention

Query Match 90.0%; Score 148.5; DB 3; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.2e-13;
Matches 33: Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVFWLRKKLODVHNY 33
 |||||

pB 1 SVSETXXXHNXGKHLNSXERVFWLRKKLODVHNY 34
 |||||

RESULT 35	
ABJ10765	
ID	ABJ10765 standard; peptide; 34 AA.
XX	
XX	ABJ10765;
XX	AC
XX	02-DEC-2002 (first entry)
DT	
XX	
DE	Human parathyroid hormone analogue #61.
XX	
KW	Human; parathyroid hormone; parathyroid hormone-related protein; PTH
KW	PTHrP; analogue; abnormal CNS function; pancreatic function;
KW	mineral metabolism; male infertility; abnormal blood pressure;
KW	hypothalamic disease.

Key	Location/Qualifiers
Modified-site	7
FT	/label= OTHER
FT	/note= "OTHER=des-Leu"
Modified-site	8
FT	/label= Nle
FT	/note= "D-form residue"
Modified-site	11
FT	/label= OTHER
FT	/note= "OTHER=cyclohexylalanine"
Modified-site	18
FT	/label= Nle
Modified-site	34
FT	/note= "C-terminal amide"
Misc-difference	34
FT	/note= "wild-type phe substituted by Tyr"

XX	WO9957139--A2.	
PN		
XX		
XX		
PD	11-NOV-1999.	
XX		
XX		
PF	03-MAY-1999; 99WO-US009521.	
XX		
XX		
PR	05-MAY-1998; 98US-00072956.	
XX		
XX	(SCRC) SOC CONSEILS RECH & APPL SCI.	
PA		
XX		
PI	Chorev M, Dong ZX, Rosenblatt M;	
XX		
DR	WPI; 2000-038790/03.	
XX		
PT	New parathyroid hormone analogs, used for treating e.g. abnormal CNS or	
PT	pancreatic functions, abnormal mineral metabolism and homeostasis, male	
PT	infertile, abnormal blood pressure or hypothalamic disease.	
PT		

XX Claim 11; Page 39; 49pp; English.

XX The present invention provides a number of parathyroid hormone (PTH) or

XX parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2

XX receptor agonists or antagonists and can be used in the treatment of

XX disorders resulting from altered or excessive action of the PTH2

XX receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,

XX divergence from normal mineral metabolism and homeostasis, male

XX infertility, abnormal blood pressure or a hypothalamic disease. The

XX present sequence is a peptide analogue of the invention

XX Sequence 34 AA;

Query Match 90.0%; Score 148.5; DB 3; Length 34;

Best Local Similarity 97.1%; Pred. No. 2.2e-13;

Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33

DB 1 SVSEIQXXHNXGKHLNSXERVELRKKLQDVHNY 34

RESULT 36

ABJ10771

ID ABJ10771 standard; peptide; 34 AA.

XX AC ABJ10771;

XX DT 02-DEC-2002 (first entry)

XX DE Human parathyroid hormone analogue #67.

XX Human; parathyroid hormone; parathyroid hormone-related protein; PTH;

XX PTHrP; analogue; abnormal CNS function; pancreatic function;

XX mineral metabolism; male infertility; abnormal blood pressure;

XX hypothalamic disease.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 8 /note= "D-form residue"

FT Modified-site 18 /label= Nle

FT Modified-site 34 /note= "C-terminal amide"

FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"

WO9557139-A2.

PN 11-NOV-1999.

PD 03-MAY-1999; 99WO-US009521.

PF 05-MAY-1998; 98US-00072956.

PR (SCRC) SOC CONSEILS RECH & APPL SCI.

PA Chorev M, Dong ZX, Rosenblatt M;

PI WPI; 2000-038790/03.

DR New parathyroid hormone analogs, used for treating e.g. abnormal CNS or

XX pancreatic functions, abnormal mineral metabolism and homeostasis, male

XX infertility, abnormal blood pressure or hypothalamic disease.

XX Claim 11; Page 40; 49pp; English.

XX The present invention provides a number of parathyroid hormone (PTH) or

XX parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2

XX receptor agonists or antagonists and can be used in the treatment of

XX disorders resulting from altered or excessive action of the PTH2

XX receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,

XX divergence from normal mineral metabolism and homeostasis, male

XX infertility, abnormal blood pressure or a hypothalamic disease. The

XX present sequence is a peptide analogue of the invention

XX Sequence 34 AA;

Query Match 90.0%; Score 148.5; DB 3; Length 34;

Best Local Similarity 94.1%; Pred. No. 2.2e-13;

Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33

DB 1 SVSEIQLXHNXGKHLNSXERVELRKKLQDVHNY 34

RESULT 37

ABJ10773

ID ABJ10773 standard; peptide; 34 AA.

XX AC ABJ10773;

XX DT 02-DEC-2002 (first entry)

XX DE Human parathyroid hormone analogue #69.

XX Human; parathyroid hormone; parathyroid hormone-related protein; PTH;

XX PTHrP; analogue; abnormal CNS function; pancreatic function;

XX mineral metabolism; male infertility; abnormal blood pressure;

XX hypothalamic disease.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 8 /label= OTHER

FT /note= "OTHER-p-benzoyl-phenylalanine, D-form residue"

FT Modified-site 34 /note= "C-terminal amide"

FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"

WO9557139-A2.

PN 11-NOV-1999.

PD 03-MAY-1999; 99WO-US009521.

PF 05-MAY-1998; 98US-00072956.

PR (SCRC) SOC CONSEILS RECH & APPL SCI.

PA Chorev M, Dong ZX, Rosenblatt M;

PI WPI; 2000-038790/03.

DR New parathyroid hormone analogs, used for treating e.g. abnormal CNS or

XX pancreatic functions, abnormal mineral metabolism and homeostasis, male

XX infertility, abnormal blood pressure or hypothalamic disease.

XX Claim 11; Page 40; 49pp; English.

XX The present invention provides a number of parathyroid hormone (PTH) or

XX parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2

XX receptor agonists or antagonists and can be used in the treatment of

XX disorders resulting from altered or excessive action of the PTH2

XX receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,

XX divergence from normal mineral metabolism and homeostasis, male

XX infertility, abnormal blood pressure or a hypothalamic disease. The

XX present sequence is a peptide analogue of the invention

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XX SQ Sequence 34 AA;
Query Match
Best Local Similarity 90.0%; Score 148.5; DB 3; Length 34;
Matches 31; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSKXRVWLRLKKLQDVHNY 33
Db 1 SVSEIQLHNLGKHLNSKXRVWLRLKKLQDVHNY 34

RESULT 38
ABJ10707
ID ABJ10707 standard; peptide; 34 AA.
XX AC ABJ10707;
XX DT 02-DEC-2002 (first entry)
XX DE Human parathyroid hormone analogue #3.
XX KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW PTHrP; analogue; abnormal CNS function; pancreatic function;
KW mineral metabolism; male infertility; abnormal blood pressure;
KW hypothalamic disease.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FT Location/Qualifiers
XX FT 8
XX FT /label= Nle
XX FT /note= "D-form residue"
XX FT 18
XX FT /label= Nle
XX FT /note= "norleucine"
XX FT 34
XX FT /note= "C-terminal amide"
XX FT Misc-difference 34
XX FT /note= "wild-type Phe substituted by Tyr"
XX PN WO9957139-A2.
XX PD 11-NOV-1999.
XX PF 03-MAY-1999; 99WO-US009521.
XX PR 05-MAY-1998; 98US-00072956.
XX PA (SCRC ) SOC CONSEILS RECH & APPL SCI.
XX PI Chorev M, Dong ZX, Rosenblatt M;
XX DR WPI; 2000-038790/03.
XX KW New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
XX PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
XX PT infertility, abnormal blood pressure or hypothalamic disease.
XX PS Claim 11; Page 38; 49pp; English.
XX CC The present invention provides a number of parathyroid hormone (PTH) or
XX CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
XX CC receptor agonists or antagonists and can be used in the treatment of
XX CC disorders resulting from altered or excessive action of the PTH2
XX CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
XX CC divergence from normal mineral metabolism and homeostasis, male
XX CC infertility, abnormal blood pressure or a hypothalamic disease. The
XX CC present sequence is a peptide analogue of the invention
XX SQ Sequence 34 AA;
Query Match
Best Local Similarity 90.0%; Score 148.5; DB 3; Length 34;
Matches 31; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSKXRVWLRLKKLQDVHNY 33
Db 1 SVSEIQLHNLGKHLNSKXRVWLRLKKLQDVHNY 34

RESULT 39
ABJ10710
ID ABJ10710 standard; peptide; 34 AA.
XX AC ABJ10710;
XX DT 02-DEC-2002 (first entry)
XX DE Human parathyroid hormone analogue #6.
XX KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW PTHrP; analogue; abnormal CNS function; pancreatic function;
KW mineral metabolism; male infertility; abnormal blood pressure;
KW hypothalamic disease.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FT Location/Qualifiers
XX FT 8
XX FT /label= OTHER
XX FT /note= "OTHER=naphthylalanine, D-form residue"
XX FT 18
XX FT /label= Nle
XX FT /note= "C-terminal amide"
XX FT 34
XX FT /note= "wild-type Phe substituted by Tyr"
XX PN WO9957139-A2.
XX PD 11-NOV-1999.
XX PF 03-MAY-1999; 99WO-US009521.
XX PR 05-MAY-1998; 98US-00072956.
XX PA (SCRC ) SOC CONSEILS RECH & APPL SCI.
XX PI Chorev M, Dong ZX, Rosenblatt M;
XX DR WPI; 2000-038790/03.
XX KW New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
XX PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
XX PT infertility, abnormal blood pressure or hypothalamic disease.
XX PS Claim 11; Page 38; 49pp; English.
XX CC The present invention provides a number of parathyroid hormone (PTH) or
XX CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
XX CC receptor agonists or antagonists and can be used in the treatment of
XX CC disorders resulting from altered or excessive action of the PTH2
XX CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
XX CC divergence from normal mineral metabolism and homeostasis, male
XX CC infertility, abnormal blood pressure or a hypothalamic disease. The
XX CC present sequence is a peptide analogue of the invention
XX SQ Sequence 34 AA;
Query Match
Best Local Similarity 90.0%; Score 148.5; DB 3; Length 34;
Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSKXRVWLRLKKLQDVHNY 33
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Job time : 138 secs

Db 1 SVSEIQLNHNGKHLNSXERVWLKKLQDVHNY 34

RESULT 40
ABJ10716
ID ABJ10716 standard; peptide; 34 AA.
XX AC ABJ10716;
XX DT 02-DEC-2002 (first entry)
XX DE Human parathyroid hormone analogue #12.
XX KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;
KW PTHrP; analogue; abnormal CNS function; pancreatic function;
KW mineral metabolism; male infertility; abnormal blood pressure;
KW hypothalamic disease.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 18
FT FT /label= Nle
FT Modified-site 34
FT FT /note= "C-terminal amide"
FT Misc-difference 34
FT FT /note= "wild-type Phe substituted by Tyr"

XX PN WO9957139-A2.
XX PD 11-NOV-1999.
XX PF 03-MAY-1999; 99WO-US009521.
XX PR 05-MAY-1998; 98US-00072956.
XX PA (SCRC) SOC CONSEILS RECH & APPL SCI.
XX PI Chorev M, Dong ZX, Rosenblatt M;
XX DR WPI; 2000-038790/03.
XX PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
PT infertility, abnormal blood pressure or hypothalamic disease.

XX PS Claim 11; Page 38; 49pp; English.
XX CC The present invention provides a number of parathyroid hormone (PTH) or
CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
CC receptor agonists or antagonists and can be used in the treatment of
CC disorders resulting from altered or excessive action of the PTH2
CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
CC divergence from normal mineral metabolism and homeostasis, male
CC infertility, abnormal blood pressure or a hypothalamic disease. The
XX present sequence is a peptide analogue of the invention
SQ Sequence 34 AA;

Query Match 90.0%; Score 148.5; DB 3; Length 34;
Best Local Similarity 91.2%; Pred. No. 2.2e-13;
Matches 31; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 SVSEIQ- XHNXGKHLNSXERVWLKKLQDVHNY 33
Db 1 SVSEIQLNHNGKHLNSXERVWLKKLQDVHNY 34

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2006, 01:09:53 ; Search time 46 Seconds
(without alignments)
59.311 Million cell updates/sec

Title: US-09-674-597A-16

Perfect score: 165

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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 - 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
 - 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	148.5	90.0	34	1	US-08-488-105-10
6	148.5	90.0	34	1	US-08-142-551B-3
7	148.5	90.0	34	2	US-08-903-497A-1
8	148.5	90.0	34	2	US-09-635-076-1
9	148.5	90.0	34	2	US-09-843-221A-21
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13	148.5	90.0	35	1	US-08-142-551B-23
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15	148.5	90.0	35	1	US-08-142-551B-32
16	148.5	90.0	35	1	US-08-142-551B-33
17	148.5	90.0	35	1	US-08-142-551B-34
18	148.5	90.0	35	1	US-08-142-551B-35
19	148.5	90.0	35	1	US-08-142-551B-36
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21	148.5	90.0	35	1	US-08-142-551B-44
22	148.5	90.0	35	1	US-08-142-551B-45
23	148.5	90.0	35	1	US-08-142-551B-46
24	148.5	90.0	35	1	US-08-142-551B-49
25	148.5	90.0	35	1	US-08-142-551B-67
26	148.5	90.0	35	1	US-08-142-551B-68
27	148.5	90.0	35	1	US-08-142-551B-70
28	148.5	90.0	35	1	US-08-142-551B-73
29	148.5	90.0	35	1	US-08-142-551B-80
30	148.5	90.0	35	1	US-08-142-551B-90
31	148.5	90.0	35	1	US-08-142-551B-94
32	148.5	90.0	44	1	US-08-468-275-4
33	148.5	90.0	44	2	US-09-007-466-4
34	148.5	90.0	44	2	US-08-952-980B-4
35	148.5	90.0	67	1	US-08-142-551B-9
36	145.5	88.2	35	1	US-08-142-551B-30
37	145.5	88.2	35	1	US-08-142-551B-50
38	145.5	88.2	35	1	US-08-142-551B-72
39	145.5	88.2	35	1	US-08-142-551B-88
40	145.5	88.2	35	1	US-08-142-551B-91
41	145.5	88.2	35	1	US-08-142-551B-95
42	145.5	88.2	35	1	US-08-142-551B-102
43	144.5	87.6	34	1	US-07-765-373-1
44	144.5	87.6	34	1	US-08-033-099-1
45	144.5	87.6	34	1	US-08-262-495C-1
46	144.5	87.6	34	1	US-07-915-247A-1
47	144.5	87.6	34	1	US-08-443-863-1
48	144.5	87.6	34	1	US-08-448-070-1
49	144.5	87.6	34	1	US-08-488-105-4
50	144.5	87.6	34	1	US-08-488-105-7
51	144.5	87.6	34	1	US-08-488-105-16
52	144.5	87.6	34	1	US-08-468-275-6
53	144.5	87.6	34	1	US-08-449-500-1
54	144.5	87.6	34	1	US-08-449-317A-1
55	144.5	87.6	34	1	US-08-142-551B-2
56	144.5	87.6	34	1	US-08-477-022-1
57	144.5	87.6	34	1	US-08-449-447-1
58	144.5	87.6	34	1	US-08-835-231-13
59	144.5	87.6	34	1	US-08-184-328-1
60	144.5	87.6	34	1	US-08-411-726-2
61	144.5	87.6	34	1	US-08-691-647C-5
62	144.5	87.6	34	1	US-08-521-097-1
63	144.5	87.6	34	2	US-09-044-536A-1
64	144.5	87.6	34	2	US-08-904-760B-22
65	144.5	87.6	34	2	US-09-108-661-13
66	144.5	87.6	34	2	US-09-007-466-6
67	144.5	87.6	34	2	US-09-406-813-1
68	144.5	87.6	34	2	US-08-952-980B-6
69	144.5	87.6	34	2	US-09-228-990-1
70	144.5	87.6	34	2	US-09-447-800-8
71	144.5	87.6	34	2	US-09-536-785A-22
72	144.5	87.6	34	2	US-09-442-989-26
73	144.5	87.6	34	2	US-09-555-447-2
74	144.5	87.6	34	2	US-09-843-221A-16
75	144.5	87.6	34	2	US-09-843-221A-17
76	144.5	87.6	34	2	US-09-843-221A-18
77	144.5	87.6	34	2	US-09-843-221A-161
78	144.5	87.6	34	2	US-09-843-221A-162
79	144.5	87.6	34	2	US-09-843-221A-163
80	144.5	87.6	34	2	US-09-555-476-2
81	144.5	87.6	34	2	US-08-903-124-1
82	144.5	87.6	34	2	US-09-623-548A-258
83	144.5	87.6	34	2	US-09-623-548A-261
84	144.5	87.6	34	2	US-09-623-548A-272
85	144.5	87.6	34	2	US-10-340-484-15
86	144.5	87.6	34	2	US-10-340-484-16
87	144.5	87.6	34	2	US-10-340-484-17
88	144.5	87.6	34	2	US-09-657-276-258
89	144.5	87.6	34	2	US-09-657-276-261
90	144.5	87.6	34	2	US-09-657-276-272
91	144.5	87.6	34	2	US-09-928-047B-6
92	144.5	87.6	34	4	PCT-US955-15800-22
93	144.5	87.6	35	1	US-08-256-363-3
94	144.5	87.6	35	1	US-08-142-551B-11
95	144.5	87.6	35	1	US-08-142-551B-12
96	144.5	87.6	35	1	US-08-142-551B-13
97	144.5	87.6	35	1	US-08-142-551B-14
98	144.5	87.6	35	1	US-08-142-551B-18
99	144.5	87.6	35	1	US-08-142-551B-20
100	144.5	87.6	35	1	US-08-142-551B-21

ALIGNMENTS

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RESULT 1
US-09-623-548A-264
; Sequence 264, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 264
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-264

Query Match          90.6%; Score 149.5; DB 2; Length 32;
Best Local Similarity 90.9%; Pred. No. 5e-14;
Matches 30; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1 SVSEIQHXNKXGKHLNSXRVWLKRLKLDVHNY 33
Db      1 SVSEIQLHNLGKHLNS-ERVWLKRLKLDVHNY 32

RESULT 2
US-09-623-548A-265
; Sequence 265, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 265
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-265

Query Match          90.6%; Score 149.5; DB 2; Length 32;
Best Local Similarity 90.9%; Pred. No. 5e-14;
Matches 30; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1 SVSEIQHXNKXGKHLNSXRVWLKRLKLDVHNY 33
Db      1 SVSEIQLHNLGKHLNS-ERVWLKRLKLDVHNY 32

RESULT 3
US-09-657-276-264
; Sequence 264, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 264
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-264

Query Match          90.6%; Score 149.5; DB 2; Length 32;
Best Local Similarity 90.9%; Pred. No. 5e-14;
Matches 30; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1 SVSEIQHXNKXGKHLNSXRVWLKRLKLDVHNY 33
Db      1 SVSEIQLHNLGKHLNS-ERVWLKRLKLDVHNY 32

RESULT 4
US-09-657-276-265
; Sequence 265, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 265
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-265

Query Match          90.6%; Score 149.5; DB 2; Length 32;
Best Local Similarity 90.9%; Pred. No. 5e-14;
Matches 30; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1 SVSEIQHXNKXGKHLNSXRVWLKRLKLDVHNY 33
Db      1 SVSEIQLHNLGKHLNS-ERVWLKRLKLDVHNY 32
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,105
FILING DATE: 07-JUN-1995
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Tsao, Y. Rocky
REGISTRATION NUMBER: 34,053
REFERENCE/DOCKET NUMBER: 00537/112001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
OTHER INFORMATION: The side chains of Lys at

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Query Match          90.0%; Score 148.5; DB 1; Length 34;
Best Local Similarity 88.2%; Pred. No. 7.3e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      1 SVSEIQ-XHNXGKHLNSXERVEWLRKKLQDVHNY 33
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Db 1 SVSEIQLHLNKGHLNSLSEVWLRKKLQDVHNY 34

RESULT 7

US-08-903-497A-1
; Sequence 1, Application US/08903497A
; Patent No. 6147186
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; TITLE OF INVENTION: No. 6147186el Parathyroid Hormone-Related
; TITLE OF INVENTION: Peptide Analogs
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/903,497A
; FILING DATE: 30-JUL-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,471
; FILING DATE: 31-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 0609.4310001/JAG/KRM
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: MODIFIED-SITE
; LOCATION: 34
; OTHER INFORMATION: CARBOXY-TERMINAL MODIFICATION OF TYROSINE-
US-08-903-497A-1

Query Match 90.0%; Score 148.5; DB 2; Length 34;
Best Local Similarity 88.2%; Pred. No. 7.3e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Db 1 SVSEIQLHLNKGHLNSLSEVWLRKKLQDVHNY 34
1 SVSEIQLHLNKGHLNSLSEVWLRKKLQDVHNY 34

RESULT 8

US-09-635-076-1
; Sequence 1, Application US/09635076
; Patent No. 6362163
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; TITLE OF INVENTION: No. 6362163el Parathyroid Hormone-Related
; TITLE OF INVENTION: Peptide Analogs
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/635,076
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/903,497
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 0609.4310001/JAG/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: MODIFIED-SITE
; LOCATION: 34
; OTHER INFORMATION: CARBOXY-TERMINAL MODIFICATION OF TYROSINE-
US-09-635-076-1

Query Match 90.0%; Score 148.5; DB 2; Length 34;
Best Local Similarity 88.2%; Pred. No. 7.3e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKXGHLNSLSEVWLRKKLQDVHNY 33
Db 1 SVSEIQLHLNKGHLNSLSEVWLRKKLQDVHNY 34

RESULT 9

US-09-843-221A-21
; Sequence 21, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: modified human PTH
US-09-843-221A-21

Query Match 90.0%; Score 148.5; DB 2; Length 34;
Best Local Similarity 88.2%; Pred. No. 7.3e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVELRKKLQDVHNY 33
Db 1 SVSEIQLLHNLGKHLNSLSEVWLRKKLQDVHNY 34

RESULT 10
US-08-142-551B-4
; Sequence 4, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is Homoserine
; OTHER INFORMATION: Lactone"
US-08-142-551B-4

Query Match 90.0%; Score 148.5; DB 1; Length 35;
Best Local Similarity 88.2%; Pred. No. 7.5e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVELRKKLQDVHNY 33

Db 1 SVSEIQLLHNLGKHLNSLSEVWLRKKLQDVHNY 34

RESULT 11
US-08-142-551B-5
; Sequence 5, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is Homoserine"
US-08-142-551B-5

Query Match 90.0%; Score 148.5; DB 1; Length 35;
Best Local Similarity 88.2%; Pred. No. 7.5e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVELRKKLQDVHNY 33
Db 1 SVSEIQLLHNLGKHLNSLSEVWLRKKLQDVHNY 34

RESULT 12
US-08-142-551B-7
; Sequence 7, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.

```
/
/ APPLICANT: Selick, Harold E.
/ TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: 699 Prince Street
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: US
/ ZIP: 22313
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/142,551B
/ FILING DATE: 25-OCT-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/077,296
/ FILING DATE: 14-JUN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/898,219
/ FILING DATE: 12-JUN-1992
/ APPLICATION NUMBER: US 07/965,677
/ FILING DATE: 22-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Swiss, Gerald F.
/ REGISTRATION NUMBER: 30,113
/ REFERENCE/DOCKET NUMBER: 000324-010
/ TELEPHONE: (415) 854-7400
/ TELEFAX: (415) 854-8275
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ NAME/KEY: Modified-site
/ LOCATION: 35
/ OTHER INFORMATION: /note= "Where "Xaa" is selected
/ OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
/ OTHER INFORMATION: amide, or the sequence of amino acids comprising
/ OTHER INFORMATION: residues 35-84 of PTH."
/
/ US-08-142-551B-7
/
/ Query Match 90.0%; Score 148.5; DB 1; Length 35;
/ Best Local Similarity 88.2%; Pred. No. 7.5e-14;
/ Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
/
/ QY 1 SVSEIQ-XHNKGKHLNSXERVWLKRLQDVHNY 33
/ Db 1 SVSEIQLLHNLGKHLNSLXERVWLKRLQDVHNY 34
/
/ RESULT 13
/ US-08-142-551B-23
/ Sequence 23, Application US/08142551B
/ Patent No. 5814603
/ GENERAL INFORMATION:
/ APPLICANT: Oldenburg, Kevin R.
/ APPLICANT: Selick, Harold E.
/ TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: 699 Prince Street
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: US
/ ZIP: 22313
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/142,551B
/ FILING DATE: 25-OCT-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/077,296
/ FILING DATE: 14-JUN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/898,219
/ FILING DATE: 12-JUN-1992
/ APPLICATION NUMBER: US 07/965,677
/ FILING DATE: 22-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Swiss, Gerald F.
/ REGISTRATION NUMBER: 30,113
/ REFERENCE/DOCKET NUMBER: 000324-010
/ TELEPHONE: (415) 854-7400
/ TELEFAX: (415) 854-8275
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ NAME/KEY: Modified-site
/ LOCATION: 35
/ OTHER INFORMATION: /note= "Where "Xaa" is selected
/ OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
/ OTHER INFORMATION: amide, or the sequence of amino acids comprising
/ OTHER INFORMATION: residues 35-84 of PTH."
/
/ US-08-142-551B-23
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/142,551B
/ FILING DATE: 25-OCT-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/077,296
/ FILING DATE: 14-JUN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/898,219
/ FILING DATE: 12-JUN-1992
/ APPLICATION NUMBER: US 07/965,677
/ FILING DATE: 22-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Swiss, Gerald F.
/ REGISTRATION NUMBER: 30,113
/ REFERENCE/DOCKET NUMBER: 000324-010
/ TELEPHONE: (415) 854-7400
/ TELEFAX: (415) 854-8275
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ NAME/KEY: Modified-site
/ LOCATION: 35
/ OTHER INFORMATION: /note= "Where "Xaa" is selected
/ OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
/ OTHER INFORMATION: amide, or the sequence of amino acids comprising
/ OTHER INFORMATION: residues 35-84 of PTH."
/
/ US-08-142-551B-23
/
/ Query Match 90.0%; Score 148.5; DB 1; Length 35;
/ Best Local Similarity 88.2%; Pred. No. 7.5e-14;
/ Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
/
/ QY 1 SVSEIQ-XHNKGKHLNSXERVWLKRLQDVHNY 33
/ Db 1 SVSEIQLLHNLGKHLNSLXERVWLKRLQDVHNY 34
/
/ RESULT 14
/ US-08-142-551B-31
/ Sequence 31, Application US/08142551B
/ Patent No. 5814603
/ GENERAL INFORMATION:
/ APPLICANT: Oldenburg, Kevin R.
/ APPLICANT: Selick, Harold E.
/ TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: 699 Prince Street
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: US
/ ZIP: 22313
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/142,551B
/ FILING DATE: 25-OCT-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/077,296
/ FILING DATE: 14-JUN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/898,219
/ FILING DATE: 12-JUN-1992
/ APPLICATION NUMBER: US 07/965,677
/ FILING DATE: 22-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Swiss, Gerald F.
/ REGISTRATION NUMBER: 30,113
/ REFERENCE/DOCKET NUMBER: 000324-010
/ TELEPHONE: (415) 854-7400
/ TELEFAX: (415) 854-8275
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ NAME/KEY: Modified-site
/ LOCATION: 35
/ OTHER INFORMATION: /note= "Where "Xaa" is selected
/ OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
/ OTHER INFORMATION: amide, or the sequence of amino acids comprising
/ OTHER INFORMATION: residues 35-84 of PTH."
/
/ US-08-142-551B-23
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; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-31,
Query Match 90.0%; Score 148.5; DB 1; Length 35;
Best Local Similarity 88.2%; Pred. No. 7.5e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHXGKHLNSXRVWLKRLQDVHNY 33
Db 1 SVSEIQKHLNGLKHLNSLSEVWLKRLQDVHNY 34

RESULT 15
US-08-142-551B-32
; Sequence 32, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400

; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
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; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
; US-08-142-551B-33
;
; Query Match 90.0%; Score 148.5; DB 1; Length 35;
; Best Local Similarity 88.2%; Pred. No. 7.5e-14;
; Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
;
; QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
; ||||| ||||| ||||| ||||| |||||
; DB 1 SVSEIQELHNLGKHLNSLSEVWLRLKQLQDVHNY 34
;
; RESULT 17
; US-08-142-551B-34
; Sequence 34, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
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; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
; US-08-142-551B-34
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; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
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; LOCATION: 35
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; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
; US-08-142-551B-33
;
; Query Match 90.0%; Score 148.5; DB 1; Length 35;
; Best Local Similarity 88.2%; Pred. No. 7.5e-14;
; Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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; QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
; ||||| ||||| ||||| ||||| |||||
; DB 1 SVSEIQELHNLGKHLNSLSEVWLRLKQLQDVHNY 34
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; RESULT 17
; US-08-142-551B-34
; Sequence 34, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
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; NAME/KEY: Modified-site
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; OTHER INFORMATION: /note= "Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
; US-08-142-551B-34
;
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 33:
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; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
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; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
; US-08-142-551B-33
;
; Query Match 90.0%; Score 148.5; DB 1; Length 35;
; Best Local Similarity 88.2%; Pred. No. 7.5e-14;
; Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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; QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
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; DB 1 SVSEIQELHNLGKHLNSLSEVWLRLKQLQDVHNY 34
;
; RESULT 17
; US-08-142-551B-34
; Sequence 34, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
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; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
; US-08-142-551B-34
;
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
; US-08-142-551B-33
;
; Query Match 90.0%; Score 148.5; DB 1; Length 35;
; Best Local Similarity 88.2%; Pred. No. 7.5e-14;
; Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
;
; QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
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; DB 1 SVSEIQELHNLGKHLNSLSEVWLRLKQLQDVHNY 34
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; RESULT 17
; US-08-142-551B-34
; Sequence 34, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
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; MOLECULE TYPE: protein
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; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
; US-08-142-551B-34
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; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of
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Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 35
OTHER INFORMATION: /note= "Where "Xaa" is selected
OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
OTHER INFORMATION: amide, or the sequence of amino acids comprising
OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-44

Query Match 90.0%; Score 148.5; DB 1; Length 35;
Best Local Similarity 88.2%; Pred. No. 7.5e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXRVWLKRLQDVHNY 33
Db 1 SVSEIQLLHNEGKHLNSLRLVWLKRLQDVHNY 34

RESULT 22
US-08-142-551B-45
Sequence 45, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
ZIP: 22313
```

```
Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 35
OTHER INFORMATION: /note= "Where "Xaa" is selected
OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
OTHER INFORMATION: amide, or the sequence of amino acids comprising
OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-45

Query Match 90.0%; Score 148.5; DB 1; Length 35;
Best Local Similarity 88.2%; Pred. No. 7.5e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXRVWLKRLQDVHNY 33
Db 1 SVSEIQLLHNEGKHLNSLRLVWLKRLQDVHNY 34

RESULT 23
US-08-142-551B-46
Sequence 46, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
ZIP: 22313
```

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/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/142,551B
/ FILING DATE: 25-OCT-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/077,296
/ FILING DATE: 14-JUN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/965,677
/ FILING DATE: 22-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Swiss, Gerald F.
/ REGISTRATION NUMBER: 30,113
/ REFERENCE/DOCKET NUMBER: 000324-010
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 854-7400
/ TELEFAX: (415) 854-8275
/ INFORMATION FOR SEQ ID NO: 46:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 35
/ OTHER INFORMATION: /note= "Xaa" is selected
/ OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
/ OTHER INFORMATION: amide, or the sequence of amino acids comprising
/ OTHER INFORMATION: residues 35-84 of PTH."
/
/ US-08-142-551B-46
/
/ Query Match 90.0%; Score 148.5; DB 1; Length 35;
/ Best Local Similarity 88.2%; Pred. No. 7.5e-14;
/ Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
/
/ QY 1 SVSEIQ-XHNXGKHLNSXRVWLKRLKLDVHNY 33
/ Db 1 SVSEIQLLHNGKHLNSLSEVWLKRLKLDVHNY 34
/
/ RESULT 24
/ US-08-142-551B-49
/ Sequence 49, Application US/08142551B
/ Patent No. 5814603
/ GENERAL INFORMATION:
/ APPLICANT: Oldenburg, Kevin R.
/ APPLICANT: Selick, Harold E.
/ TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
/ TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: 699 Prince Street
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: US
/ ZIP: 22313
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/142,551B
```

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/
/ FILING DATE: 25-OCT-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/077,296
/ FILING DATE: 14-JUN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/898,219
/ FILING DATE: 12-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/965,677
/ FILING DATE: 22-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Swiss, Gerald F.
/ REGISTRATION NUMBER: 30,113
/ REFERENCE/DOCKET NUMBER: 000324-010
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 854-7400
/ TELEFAX: (415) 854-8275
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 35
/ OTHER INFORMATION: /note= "Xaa" is selected
/ OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
/ OTHER INFORMATION: amide, or the sequence of amino acids comprising
/ OTHER INFORMATION: residues 35-84 of PTH."
/
/ US-08-142-551B-49
/
/ Query Match 90.0%; Score 148.5; DB 1; Length 35;
/ Best Local Similarity 88.2%; Pred. No. 7.5e-14;
/ Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
/
/ QY 1 SVSEIQ-XHNXGKHLNSXRVWLKRLKLDVHNY 33
/ Db 1 SVSEIQLLHNGKHLNSLSEVWLKRLKLDVHNY 34
/
/ RESULT 25
/ US-08-142-551B-67
/ Sequence 67, Application US/08142551B
/ Patent No. 5814603
/ GENERAL INFORMATION:
/ APPLICANT: Oldenburg, Kevin R.
/ APPLICANT: Selick, Harold E.
/ TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
/ TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: 699 Prince Street
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: US
/ ZIP: 22313
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/142,551B
/ FILING DATE: 25-OCT-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/077,296
/ FILING DATE: 14-JUN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/898,219
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/ FILING DATE: 12-JUN-1992
/ PRIOR APPLICATION DATA: US 07/965,677
/ APPLICATION NUMBER: US 07/965,677
/ FILING DATE: 22-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Swiss, Gerald F.
/ REGISTRATION NUMBER: 30,113
/ REFERENCE/DOCKET NUMBER: 000324-010
/ TELEPHONE: (415) 854-7400
/ TELEFAX: (415) 854-8275
/ INFORMATION FOR SEQ ID NO: 67:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 35
/ OTHER INFORMATION: /note= "Where "Xaa" is selected
/ OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
/ OTHER INFORMATION: amide, or the sequence of amino acids comprising
/ OTHER INFORMATION: residues 35-84 of PTH."
/
US-08-142-551B-67

Query Match 90.0%; Score 148.5; DB 1; Length 35;
Best Local Similarity 88.2%; Pred. No. 7.5e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXRVWLKRLQDVHNY 33
Db 1 SVSEIQLLHNLGKHLNSRVERWLKRLQDVHNY 34

RESULT 26
US-08-142-551B-68
/ Sequence 68, Application US/08142551B
/ Patent No. 5814603
/ GENERAL INFORMATION:
/ APPLICANT: Oldenburg, Kevin R.
/ APPLICANT: Selick, Harold E.
/ TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
/ TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: 699 Prince Street
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: US
/ ZIP: 22313
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 25-OCT-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/077,296
/ FILING DATE: 14-JUN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/898,219
/ FILING DATE: 12-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/965,677
/ FILING DATE: 22-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Swiss, Gerald F.
/ REGISTRATION NUMBER: 30,113
/ REFERENCE/DOCKET NUMBER: 000324-010
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 854-7400
/ TELEFAX: (415) 854-8275
/ INFORMATION FOR SEQ ID NO: 70:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35 amino acids
/

QY 1 SVSEIQ-XHNKGKHLNSXRVWLKRLQDVHNY 33
Db 1 SVSEIQLLHNLGKHLNSRVERWLKRLQDVHNY 34

RESULT 27
US-08-142-551B-70
/ Sequence 70, Application US/08142551B
/ Patent No. 5814603
/ GENERAL INFORMATION:
/ APPLICANT: Oldenburg, Kevin R.
/ APPLICANT: Selick, Harold E.
/ TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
/ TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: 699 Prince Street
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: US
/ ZIP: 22313
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/142,551B
/ FILING DATE: 25-OCT-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/077,296
/ FILING DATE: 14-JUN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/898,219
/ FILING DATE: 12-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/965,677
/ FILING DATE: 22-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Swiss, Gerald F.
/ REGISTRATION NUMBER: 30,113
/ REFERENCE/DOCKET NUMBER: 000324-010
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 854-7400
/ TELEFAX: (415) 854-8275
/ INFORMATION FOR SEQ ID NO: 70:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35 amino acids
/
```

;
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-70

Query Match 90.0%; Score 148.5; DB 1; Length 35;
Best Local Similarity 88.2%; Pred. No. 7.5e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
Db 1 SVSEIQLLHNLGKHLNSLSEVWLRRKKLQDVHNY 34

RESULT 28
US-08-142-551B-73
; Sequence 73, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected

;
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-73

Query Match 90.0%; Score 148.5; DB 1; Length 35;
Best Local Similarity 88.2%; Pred. No. 7.5e-14;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVELRKKLQDVHNY 33
Db 1 SVSEIQLLHNLGKHLNSLSEVWLRRKKLQDVHNY 34

RESULT 29
US-08-142-551B-80
; Sequence 80, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-80

Query Match 90.0%; Score 148.5; DB 1; Length 35;
Best Local Similarity 88.2%; Pred. No. 7.5e-14;


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1  TITLE OF INVENTION:  METHOD FOR INCREASING THE
2  TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
3  NUMBER OF SEQUENCES:  10
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  ALZA CORPORATION
6  STREET:  950 PAGE MILL ROAD
7  CITY:  PALO ALTO
8  STATE:  CALIFORNIA
9  COUNTRY:  USA
10 ZIP:  94303-0802
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE:  Floppy disk
13 COMPUTER:  IBM PC compatible
14 OPERATING SYSTEM:  PC-DOS/MS-DOS
15 SOFTWARE:  PatentIn Release #1.0, Version #1.30
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER:  US/08/468,275
18 FILING DATE:  06-JUN-1995
19 CLASSIFICATION:  514
20 ATTORNEY/AGENT INFORMATION:
21 NAME:  MILLER, D. BYRON
22 REGISTRATION NUMBER:  30,661
23 REFERENCE/DOCKET NUMBER:  O360-0002; ARC-2349
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE:  (415) 496-8150
26 TELEFAX:  (415) 496-8048
27 INFORMATION FOR SEQ ID NO:  4:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH:  44 amino acids
30 TYPE:  amino acid
31 TOPOLOGY:  linear
32 MOLECULE TYPE:  protein
33 US-08-468-275-4

```

```

; NAME: MILLER, D. BYRON
; REGISTRATION NUMBER: 30,661
; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 496-8150
; TELEFAX: (415) 496-8048
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-007-466-4

Query Match          90.0%; Score 148.5; DB 2; Length 44;
Best Local Similarity 88.2%; Pred. No. 9.6e-14;
Matches 30; Conservative 0; Mismatches 3; Indels

Qy 1 SVSEIQ-XHNKGKHLNSKXRVWLKKLQDVHNY 33
Db 7 SVSEIQLLHNLGKHLNSLSEVWLKKLQDVHNY 40

RESULT 34
US-08-952-980B-4
; Sequence 4, Application US/08952980B
; Patent No. 633189
; GENERAL INFORMATION:
; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALZA CORPORATION
; STREET: 950 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94303-0802
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,980B
; FILING DATE: 20-NOV-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLER, D. BYRON
; REGISTRATION NUMBER: 30,661
; REFERENCE/DOCKET NUMBER: 2349 CIP 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 496-8150
; TELEFAX: (650) 496-8048
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-952-980B-4

Query Match          90.0%; Score 148.5; DB 2; Length 44;
Best Local Similarity 88.2%; Pred. No. 9.6e-14;
Matches 30; Conservative 0; Mismatches 3; Indels

Qy 1 SVSEIQ-XHNKGKHLNSKXRVWLKKLQDVHNY 33
Db 7 SVSEIQLLHNLGKHLNSLSEVWLKKLQDVHNY 40

```

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RESULT 35
US-08-142-551B-9
; Sequence 9, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-142-551B-9

Query Match          90.0%; Score 148.5; DB 1; Length 67;
Best Local Similarity 88.2%; Pred. No. 1.5e-13;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      1 SVSEIQ-XHNKGKHLNSXRVWLKRLKQDVHNY 33
Db      24 SVSEIQLLHNLGKHLNSLRLVWLKRLKQDVHNY 57

RESULT 36
US-08-142-551B-30
; Sequence 30, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
```

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; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note="Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-30

Query Match          88.2%; Score 145.5; DB 1; Length 35;
Best Local Similarity 85.3%; Pred. No. 2e-13;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy      1 SVSEIQ-XHNKGKHLNSXRVWLKRLKQDVHNY 33
Db      1 SVSEIQLLHNLGKHLNSLRLVWLKRLKQDVHNY 34

RESULT 37
US-08-142-551B-50
; Sequence 50, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-88

Query Match      88.2%; Score 145.5; DB 1; Length 35;
Best Local Similarity 85.3%; Pred. No. 2e-13;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGHLNSXERVELRKQLQDVHNY 33
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Db 1 SVSEIQLLHNLGKHLNSLSEVWLRLKKLQDVHNY 34
    ||||| ||||| ||||| ||||| |||||

RESULT 40
US-08-142-551B-91
; Sequence 91, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Qidenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
```

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; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-91
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Query Match      88.2%; Score 145.5; DB 1; Length 35;
Best Local Similarity 85.3%; Pred. No. 2e-13;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGHLNSXERVELRKQLQDVHNY 33
    ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQLLHNLGKHLNSLSEVWLRLKKLQDVHNY 34
    ||||| ||||| ||||| ||||| |||||
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Search completed: January 28, 2006, 01:17:38
Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2006, 01:16:04 ; Search time 62 Seconds
(without alignments)
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Title: US-09-674-597A-16

Perfect score: 165

Sequence: 1 SVSEIQXHNXGKHLNSXERVWLKKLODVHNY 33

Scoring table: BLOSUM62

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149.5	90.6	32	6	US-11-066-697-264
2	149.5	90.6	32	6	US-11-066-697-265
3	148.5	90.0	34	3	US-09-843-221A-21
4	148.5	90.0	34	3	US-09-999-608-21
5	148.5	90.0	34	4	US-10-311-366-15
6	148.5	90.0	34	4	US-10-839-037-21
7	148.5	90.0	34	5	US-10-428-377-45
8	148.5	90.0	34	5	US-10-718-071-14
9	144.5	87.6	34	3	US-09-169-786-3
10	144.5	87.6	34	3	US-09-858-880-5
11	144.5	87.6	34	3	US-09-928-047B-6
12	144.5	87.6	34	3	US-09-843-221A-16
13	144.5	87.6	34	3	US-09-843-221A-17
14	144.5	87.6	34	3	US-09-843-221A-18
15	144.5	87.6	34	3	US-09-843-221A-161
16	144.5	87.6	34	3	US-09-843-221A-162
17	144.5	87.6	34	3	US-09-843-221A-163
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21	144.5	87.6	34	3	US-09-999-608-18
22	144.5	87.6	34	3	US-09-999-608-161
23	144.5	87.6	34	3	US-09-999-608-162
24	144.5	87.6	34	3	US-09-999-608-163
25	144.5	87.6	34	4	US-10-016-403-5
26	144.5	87.6	34	4	US-10-097-079-1
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44	144.5	87.6	34	5	US-10-428-377-29
45	144.5	87.6	34	5	US-10-638-265-82
46	144.5	87.6	34	5	US-10-892-025-4
47	144.5	87.6	34	5	US-10-312-726A-2
48	144.5	87.6	34	5	US-10-775-204-456
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61	144.5	87.6	35	6	US-11-066-697-286
62	144.5	87.6	36	5	US-10-892-025-6
63	144.5	87.6	37	4	US-10-168-185-9
64	144.5	87.6	37	5	US-10-466-483A-8
65	144.5	87.6	37	5	US-10-892-025-7
66	144.5	87.6	37	5	US-10-997-078-41
67	144.5	87.6	37	5	US-10-997-700-14
68	144.5	87.6	38	3	US-09-169-786-4
69	144.5	87.6	38	3	US-09-843-221A-14
70	144.5	87.6	38	3	US-09-999-608-14
71	144.5	87.6	38	4	US-10-245-707-1
72	144.5	87.6	38	4	US-10-398-449-20
73	144.5	87.6	38	4	US-10-311-366-18
74	144.5	87.6	38	5	US-10-839-037-14
75	144.5	87.6	38	5	US-10-892-025-8
76	144.5	87.6	39	6	US-11-066-697-275
77	144.5	87.6	40	5	US-10-892-025-9
78	144.5	87.6	41	5	US-10-892-025-10
79	144.5	87.6	42	4	US-10-024-918-28
80	144.5	87.6	42	4	US-10-325-021-17
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83	144.5	87.6	42	5	US-10-892-025-12
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85	144.5	87.6	44	3	US-09-843-221A-13
86	144.5	87.6	44	3	US-09-999-608-13
87	144.5	87.6	44	4	US-10-398-449-44
88	144.5	87.6	44	4	US-10-311-366-19
89	144.5	87.6	44	4	US-10-839-037-13
90	144.5	87.6	44	5	US-11-066-697-276
91	144.5	87.6	45	6	US-11-066-697-285
92	144.5	87.6	46	4	US-10-325-021-18
93	144.5	87.6	46	4	Sequence 1, Appl
94	144.5	87.6	46	4	Sequence 2, Appl
95	144.5	87.6	46	4	Sequence 3, Appl
96	144.5	87.6	46	4	Sequence 4, Appl
97	144.5	87.6	46	4	Sequence 5, Appl
98	144.5	87.6	46	4	Sequence 6, Appl
99	144.5	87.6	46	4	Sequence 7, Appl
100	144.5	87.6	46	4	Sequence 8, Appl

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ALIGNMENTS

RESULT 1
US-11-066-697-264
; Sequence 264, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 264
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-264

Query Match          90.6%; Score 149.5; DB 6; Length 32;
Best Local Similarity 90.9%; Pred. No. 1.9e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 SVSEIQXHNKXGKHLNSXERVWLKRLQDVHNY 33
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Db 1 SVSEIQLHNLGKHLNS-ERVWLKRLQDVHNY 32

RESULT 2
US-11-066-697-265
; Sequence 265, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 265
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-265

Query Match          90.6%; Score 149.5; DB 6; Length 32;
Best Local Similarity 90.9%; Pred. No. 1.9e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 SVSEIQXHNKXGKHLNSXERVWLKRLQDVHNY 33
    ||||| ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQLHNLGKHLNS-ERVWLKRLQDVHNY 32

RESULT 3
US-09-843-221A-21
; Sequence 21, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-21

Query Match          90.0%; Score 148.5; DB 3; Length 34;
Best Local Similarity 88.2%; Pred. No. 2.8e-13;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSXERVWLKRLQDVHNY 33
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Db 1 SVSEIQLHNLGKHLNS-ERVWLKRLQDVHNY 34

RESULT 4
US-09-999-608-21
; Sequence 21, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: GEGG, COLIN V.
; APPLICANT: JAROSINSKI, MARK ANTHONY
; APPLICANT: KINSTLER, OLAF BORIS
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: HORMONE-RELATED PROTEIN
; FILE REFERENCE: A-665C
; CURRENT APPLICATION NUMBER: US/09/999,608
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/843,221
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/214,860
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; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-999-608-21

Query Match 90.0%; Score 148.5; DB 3; Length 34;
Best Local Similarity 88.2%; Pred. No. 2.8e-13;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVEWLKRLKQDVHNY 33
Db 1 SVSEIQLHLNGLKHLNSLSEVWLKRLKQDVHNY 34

RESULT 5

US-10-311-366-15
; Sequence 15, Application US/10311366
; Publication No. US20040022838A1
; GENERAL INFORMATION:

; APPLICANT: Holick, Michael F.
; TITLE OF INVENTION: Regulation Of Cell Proliferation And Differentiation Using Topical
; FILE REFERENCE: 1539.0310001
; CURRENT APPLICATION NUMBER: US/10/311,366
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19650
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/213,247
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; NAME/KEY: MOD RES
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; OTHER INFORMATION: Nle
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (18)..(18)
; OTHER INFORMATION: Nle
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: [Nle8,18, Tyr34] hPTH (1-34)

US-10-311-366-15

Query Match 90.0%; Score 148.5; DB 4; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.8e-13;
Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVEWLKRLKQDVHNY 33
Db 1 SVSEIQLHLNGLKHLNSXERVEWLKRLKQDVHNY 34

RESULT 6

US-10-839-037-21
; Sequence 21, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE

;
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/10/839,037
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-10-839-037-21

Query Match 90.0%; Score 148.5; DB 4; Length 34;
Best Local Similarity 88.2%; Pred. No. 2.8e-13;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVEWLKRLKQDVHNY 33
Db 1 SVSEIQLHLNGLKHLNSLSEVWLKRLKQDVHNY 34

RESULT 7

US-10-428-377-45
; Sequence 45, Application US/10428377
; Publication No. US20040220094A1
; GENERAL INFORMATION:

; APPLICANT: Skinner, Keith
; TITLE OF INVENTION: INVERSE AGONIST AND AGONIST PEPTIDES
; FILE REFERENCE: 549042000100
; CURRENT APPLICATION NUMBER: US/10/428,377
; CURRENT FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 8
; OTHER INFORMATION: Nle
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 18
; OTHER INFORMATION: Nle
; OTHER INFORMATION: Nle
US-10-428-377-45

Query Match 90.0%; Score 148.5; DB 5; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.8e-13;
Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVEWLKRLKQDVHNY 33
Db 1 SVSEIQLHLNGLKHLNSXERVEWLKRLKQDVHNY 34

RESULT 8

US-10-718-071-14
; Sequence 14, Application US/10718071
; Publication No. US20050009847A1
; GENERAL INFORMATION:

```
; APPLICANT: Bertilsson, Goran
; APPLICANT: Erlandsson, Rikard
; APPLICANT: Frisen, Jonas
; APPLICANT: Haegerstrand, Anders
; APPLICANT: Heidrich, Jessica
; APPLICANT: Hellstrom, Kristina
; APPLICANT: Hagglad, Johan
; APPLICANT: Jansson, Katarina
; APPLICANT: Korteasaa, Jarkko
; APPLICANT: Lindquist, Per
; APPLICANT: Lundh, Hanna
; APPLICANT: McGuire, Jacqueline
; APPLICANT: Mercer, Alex
; APPLICANT: Nyberg, Karl
; APPLICANT: Ossolinak, Anina
; APPLICANT: Patrone, Cesare
; APPLICANT: Ronnholm, Harriet
; APPLICANT: Warkstrom, Lillian
; APPLICANT: Zachrisson, Olof
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INCREASING NEUROGENESIS
; FILE REFERENCE: 21882-517 UTIL
; CURRENT APPLICATION NUMBER: US/10/718,071
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US 60/427,912
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: norleucine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: norleucine
US-10-718-071-14
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```
Query Match 90.0%; Score 148.5; DB 5; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.8e-13;
Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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*QY 1 SVSEIQ-XHNKGKHLNSXERVWLRKKLQDVHNY 33
Db 1 SVSEIQLMHNGLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 9
US-09-169-786-3
; Sequence 3, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-3
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Query Match 87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
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```
QY 1 SVSEIQ-XHNKGKHLNSXERVWLRKKLQDVHNY 33
Db 1 SVSEIQLMHNGLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 10
US-09-858-880-5
; Sequence 5, Application US/0985880
; Publication No. US20020061838A1
; GENERAL INFORMATION:
; APPLICANT: Holmquist, Barton
; APPLICANT: Dormady, Daniel
; TITLE OF INVENTION: Peptide Pharmaceutical Formulations
; FILE REFERENCE: 1627.020US1
; CURRENT APPLICATION NUMBER: US/09/858,880
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205,377
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: US 60/205,262
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-880-5
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```
Query Match 87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
```

```
QY 1 SVSEIQ-XHNKGKHLNSXERVWLRKKLQDVHNY 33
Db 1 SVSEIQLMHNGLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 11
US-09-928-047B-6
; Sequence 6, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-6
```

```
Query Match 87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
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```
QY 1 SVSEIQ-XHNKGKHLNSXERVWLRKKLQDVHNY 33
Db 1 SVSEIQLMHNGLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 12
US-09-843-221A-16
; Sequence 16, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
```

; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-16

Query Match 87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33
||||| ||||||| ||||||| ||||||| |||||||
DB 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 13
US-09-843-221A-17
; Sequence 17, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-17

Query Match 87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33
||||| ||||||| ||||||| ||||||| |||||||
DB 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14
US-09-843-221A-18
; Sequence 18, Application US/09843221A
; Publication No. US20030039654A1

; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID ;
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-18

Query Match 87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33
||||| ||||||| ||||||| ||||||| |||||||
DB 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 15
US-09-843-221A-161
; Sequence 161, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID I
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc feature
; LOCATION: (34)...(34)
; OTHER INFORMATION: Optional linker and Pc domain attached at the C-terminus
US-09-843-221A-161

Query Match 87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33
||||| ||||||| ||||||| ||||||| |||||||
DB 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 16
 US-09-843-221A-162
 ; Sequence 162, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843, 221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/286, 673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214, 860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200, 053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 162
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Preferred embodiments - PTH
 ; NAME/KEY: misc_feature
 ; LOCATION: (34)..(34)
 ; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
 US-09-843-221A-162

Query Match	87.6%	Score 144.5	DB 3	Length 34
Best Local Similarity	85.3%	Pred. No. 1e-12		
Matches 29	Conservative	1	Mismatches 3	Indels 1
Gaps				1
QY	1	SVSEIQ-XHXGKHLNSXERVELWLRKQLQDVHNY	33	
, Db	1	SVSEIQLMENRGKHLNSXERVELWLRKQLQDVHNF	34	

RESULT 17
US-09-843-221A-163
• Sequence 163, Application US/09843221A
; Publication No. US200300396541
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843.221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc feature
; LOCATION: (34)-(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

```

US-09-843-201A-163

Query Match      87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSKERVWLRKKLQDVHNY 33
Db 1 SVSEIQ-LMHNKGLHNSMERVWLRKKLQDVHNF 34

RESULT 18
US-09-928-048A-6
; Sequence 6, Application US/09928048A
; Publication No. US20030138858A1
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-6

Query Match      87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSKERVWLRKKLQDVHNY 33
Db 1 SVSEIQ-LMHNKGLHNSMERVWLRKKLQDVHNF 34

```

RESULT 19

US-09-999-608-16

; Sequence 16, Application US/09999608

; Publication No. US20050124537A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUK, PAUL

; APPLICANT: GEGG, COLIN V.

; APPLICANT: JAROSINSKI, MARK ANTHONY

; APPLICANT: KINSTLER, OLAF BORIS

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID

; TITLE OF INVENTION: HORMONE-RELATED PROTEIN

; FILE REFERENCE: A-665C

; CURRENT APPLICATION NUMBER: US/09/999,608

; CURRENT FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 09/843,221

; PRIOR FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: US 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: US 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: US 60/200,053

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 193

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 16

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-999-608-16

Query Match 87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;


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; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/843,221
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-999-608-162

Query Match      87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSXERVEWLKKLQDVHNF 33
Db 1 SVSEIQLMHNKGLHNSMVERVWLKKLQDVHNF 34

RESULT 24
US-09-999-608-163
; Sequence 163, Application US/09999608
; Publication No. US20050124537A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: GEGG, COLIN V.
; APPLICANT: JAROSINSKI, MARK ANTHONY
; APPLICANT: KINSTLER, OLAF BORIS
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: HORMONE-RELATED PROTEIN
; FILE REFERENCE: A-665C
; CURRENT APPLICATION NUMBER: US/09/999,608
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/843,221
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-999-608-163

Query Match      87.6%; Score 144.5; DB 3; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSXERVEWLKKLQDVHNF 33
Db 1 SVSEIQLMHNKGLHNSMVERVWLKKLQDVHNF 34
```

```
Db 1 SVSEIQLMHNKGLHNSMVERVWLKKLQDVHNF 34

RESULT 25
US-10-016-403-5
; Sequence 5, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "parathyroid hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-016-403-5

Query Match      87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSXERVEWLKKLQDVHNF 33
Db 1 SVSEIQLMHNKGLHNSMVERVWLKKLQDVHNF 34

RESULT 26
US-10-097-079-1
; Sequence 1, Application US/10097079
; Publication No. US20020132973A1
; GENERAL INFORMATION:
; APPLICANT: Condon, Stephen M.
; Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
```

STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/097,079
FILING DATE: 13-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/228,990
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/046,472
FILING DATE: 14-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Martin Esq., Michael B.
REGISTRATION NUMBER: 37,521
REFERENCE/DOCKET NUMBER: A2678B-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-2793
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: No. US20020132973A1 Relevant
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-097-079-1

Query Match 87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVWLKKLQDVHNY 33
DB 1 SVSEIQLMHNLGKHLNSMERVWLKKLQDVHNF 34

RESULT 27
US-10-361-928-8
Sequence 8, Application US/10361928
Publication No. US20030144209A1
GENERAL INFORMATION:
APPLICANT: BRINGHURST, F. RICHARD
APPLICANT: TAKASU, HISASHI
APPLICANT: GARDELLA, THOMAS J.
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: ANALOGS
FILE REFERENCE: 0609.463002
CURRENT APPLICATION NUMBER: US/10/361,928
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: 09/447,800
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/110,152
PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)_
OTHER INFORMATION: Desamino Ser
US-10-361-928-8

Query Match 87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 1 SVSEIQ-XHNKGKHLNSXERVWLKKLQDVHNY 33
DB 1 SVSEIQLMHNLGKHLNSMERVWLKKLQDVHNF 34
RESULT 28
US-10-340-484-15
Sequence 15, Application US/10340484
Publication No. US20030171288A1
GENERAL INFORMATION:
APPLICANT: Stewart, Andrew F.
TITLE OF INVENTION: Treatment of Bone Disorders with Skeletal Anabolic
TITLE OF INVENTION: Drugs
FILE REFERENCE: 25200-501
CURRENT APPLICATION NUMBER: US/10/340,484
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 60/347,215
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 60/353,296
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 60/368,955
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/379,125
PRIOR FILING DATE: 2002-05-08
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-10-340-484-15

Query Match 87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVWLKKLQDVHNY 33
DB 1 SVSEIQLMHNLGKHLNSMERVWLKKLQDVHNF 34

RESULT 29
US-10-340-484-16
Sequence 16, Application US/10340484
Publication No. US20030171288A1
GENERAL INFORMATION:
APPLICANT: Stewart, Andrew F.
TITLE OF INVENTION: Treatment of Bone Disorders with Skeletal Anabolic
TITLE OF INVENTION: Drugs
FILE REFERENCE: 25200-501
CURRENT APPLICATION NUMBER: US/10/340,484
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 60/347,215
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 60/353,296
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 60/368,955
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/379,125
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 34
TYPE: PRT
ORGANISM: Macaca fascicularis
US-10-340-484-16
Query Match 87.6%; Score 144.5; DB 4; Length 34;

Best Local Similarity 85.3%; Pred. No. 1e-12; DB 4; Length 34;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSXERVEWLRKKLQDVHNY 33
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 30

US-10-340-484-17
; Sequence 17, Application US/10340484
; Publication No. US20030171289A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skeletal Anabolic
; FILE REFERENCE: 1539.0320001
; CURRENT APPLICATION NUMBER: US/10/340,484
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-340-484-17

Query Match 87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 31

US-10-427-259-2
; Sequence 2, Application US/10427259
; Publication No. US20030225000A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Chin-Ming
; TITLE OF INVENTION: Stabilized Teriparatide Solutions
; FILE REFERENCE: X-10911B
; CURRENT APPLICATION NUMBER: US/10/427,259
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-427-259-2

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Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 32

US-10-398-449-14
; Sequence 14, Application US/10398449
; Publication No. US20040013719A1
; GENERAL INFORMATION:
; APPLICANT: Hollick, Michael F.
; TITLE OF INVENTION: Regulation of Cell Proliferation And Differentiation
; FILE REFERENCE: 1539.0320001
; CURRENT APPLICATION NUMBER: US/10/398,449
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: PCT/US01/31082
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 60/238,134
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: hPTH (1-34)
US-10-398-449-14

Query Match 87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSXERVEWLRKKLQDVHNY 33
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 33

US-10-398-449-18
; Sequence 18, Application US/10398449
; Publication No. US20040013719A1
; GENERAL INFORMATION:
; APPLICANT: Hollick, Michael F.
; TITLE OF INVENTION: Regulation of Cell Proliferation And Differentiation
; FILE REFERENCE: 1539.0320001
; CURRENT APPLICATION NUMBER: US/10/398,449
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: PCT/US01/31082
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 60/238,134
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: hPTH (1-34)
US-10-398-449-18

Query Match 87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSXERVEWLRKKLQDVHNY 33
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 34

US-10-311-366-13
; Sequence 13, Application US/10311366
; Publication No. US20040022838A1
; GENERAL INFORMATION:
; APPLICANT: Hollick, Michael F.

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; TITLE OF INVENTION: Regulation of Cell Proliferation And Differentiation Using Topical
; FILE REFERENCE: Applied Peptides
; CURRENT APPLICATION NUMBER: 1539.0310001
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/10/311,366
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19650
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/213,247
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: hPTH (1-34)
US-10-311-366-13

Query Match      87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVWLKKLQDVHNY 33
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Db 1 SVSEIQLMHNLGKHLNSMERVWLKKLQDVHNF 34

RESULT 35
US-10-440-473-1
; Sequence 1, Application US/10440473
; Publication No. US20040023892A1
; GENERAL INFORMATION:
; APPLICANT: PERI, KRISHNA G.
; APPLICANT: HIGH, KIM
; APPLICANT: BERGERON, ANNIE
; APPLICANT: MOFFETT, SERGE
; APPLICANT: ABRIBAT, THIERRY
; TITLE OF INVENTION: PTH DERIVATIVES RESISTANT TO SKIN PROTEASES
; FILE REFERENCE: GOURD:029US
; CURRENT APPLICATION NUMBER: US/10/440,473
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/378,072
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-440-473-1

Query Match      87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
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Db 1 SVSEIQLMHNLGKHLNSMERVWLKKLQDVHNF 34

RESULT 36
US-10-443-693-2
; Sequence 2, Application US/10443693
; Publication No. US20040033950A1
; GENERAL INFORMATION:
; APPLICANT: Hock, Janet
; APPLICANT: Gaich, Gregory
; APPLICANT: Dere, Willard
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; TITLE OF INVENTION: Method of Increasing Bone Toughness and Stiffness and Reducing F
; FILE REFERENCE: X-11965A
; CURRENT APPLICATION NUMBER: US/10/443,693
; CURRENT FILING DATE: 2003-05-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(34)
; OTHER INFORMATION:
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Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVWLKKLQDVHNY 33
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Db 1 SVSEIQLMHNLGKHLNSMERVWLKKLQDVHNF 34

RESULT 37
US-10-343-189-16
; Sequence 16, Application US/10343189
; Publication No. US20040214271A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Takashi
; APPLICANT: KOBAYASHI, Masayuki
; APPLICANT: SAWADA, Hidekazu
; TITLE OF INVENTION: Method of Culture for Recombinant Escherichia coli.
; FILE REFERENCE: 2765 USOP
; CURRENT APPLICATION NUMBER: US/10/343,189
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: PCT/JP01/06531
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: JP 2000-232389
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Human
US-10-343-189-16

Query Match 87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVWLKKLQDVHNY 33
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Db 1 SVSEIQLMHNLGKHLNSMERVWLKKLQDVHNF 34

RESULT 38
US-10-839-037-16
; Sequence 16, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/10/839,037
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673

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; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-839-037-16

Query Match      87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSKXERVWLKRLKLDVHNY 33
DB 1 SVSEIQLMHNKLGKHLNSMERVWLKRLKLDVHNF 34

RESULT 39
US-10-839-037-17
; Sequence 17, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/10/839,037
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-10-839-037-17

Query Match      87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSKXERVWLKRLKLDVHNY 33
DB 1 SVSEIQLMHNKLGKHLNSMERVWLKRLKLDVHNF 34

RESULT 40
US-10-839-037-18
; Sequence 18, Application US/10839037
; Publication No. US20040214996A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
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; CURRENT APPLICATION NUMBER: US/10/839,037
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-10-839-037-18
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Query Match      87.6%; Score 144.5; DB 4; Length 34;
Best Local Similarity 85.3%; Pred. No. 1e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSKXERVWLKRLKLDVHNY 33
DB 1 SVSEIQLMHNKLGKHLNSMERVWLKRLKLDVHNF 34
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Search completed: January 28, 2006, 01:28:27
Job time : 64 secs

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OM protein - protein search, using sw model

Run on: January 28, 2006, 01:26:16 ; Search time 8 Seconds
(without alignments)
44.670 Million cell updates/sec

Title: US-09-674-597A-16

Perfect score: 165

Sequence: 1 SVSEIQXHNXKHLNSXERVWLKKLQDVHNY 33

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Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications_AA_New.*

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2: /cgn2_6/prodata/2/pubaa/US06_NEW_PUB.pep.*

3: /cgn2_6/prodata/2/pubaa/US07_NEW_PUB.pep.*

4: /cgn2_6/prodata/2/pubaa/PCT_NEW_PUB.pep.*

5: /cgn2_6/prodata/2/pubaa/US05_NEW_PUB.pep.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148.5	90.0	34	7 US-11-035-826-37	Sequence 37, Appl
2	148.5	90.0	34	7 US-11-035-826-192	Sequence 192, Appl
3	144.5	87.6	34	7 US-11-176-735-19	Sequence 19, Appl
4	144.5	87.6	34	7 US-11-126-996-2	Sequence 2, Appl
5	144.5	87.6	34	7 US-11-035-826-18	Sequence 18, Appl
6	144.5	87.6	34	7 US-11-035-826-33	Sequence 33, Appl
7	144.5	87.6	34	7 US-11-035-826-34	Sequence 34, Appl
8	144.5	87.6	34	7 US-11-035-826-36	Sequence 36, Appl
9	144.5	87.6	34	7 US-11-035-826-67	Sequence 67, Appl
10	144.5	87.6	34	7 US-11-035-826-78	Sequence 78, Appl
11	144.5	87.6	34	7 US-11-035-826-97	Sequence 97, Appl
12	144.5	87.6	34	7 US-11-035-826-98	Sequence 98, Appl
13	144.5	87.6	34	7 US-11-035-826-186	Sequence 186, Appl
14	144.5	87.6	34	7 US-11-035-826-189	Sequence 189, Appl
15	144.5	87.6	34	7 US-11-035-826-198	Sequence 198, Appl
16	144.5	87.6	36	7 US-11-035-826-20	Sequence 20, Appl
17	144.5	87.6	37	7 US-11-035-826-19	Sequence 19, Appl
18	144.5	87.6	84	7 US-11-126-996-1	Sequence 1, Appl
19	144.5	87.6	84	7 US-11-035-826-15	Sequence 15, Appl
20	143.5	87.0	34	7 US-11-035-826-99	Sequence 99, Appl
21	142.5	86.4	34	7 US-11-035-826-85	Sequence 85, Appl
22	141.5	85.8	34	7 US-11-035-826-50	Sequence 50, Appl
23	141.5	85.8	34	7 US-11-035-826-59	Sequence 59, Appl
24	141.5	85.8	34	7 US-11-035-826-60	Sequence 60, Appl
25	141.5	85.8	34	7 US-11-035-826-66	Sequence 66, Appl

Sequence 76, Appl	7	US-11-035-826-76	34	85.8	141.5	26
Sequence 260, App	34	7 US-11-035-826-260	34	85.8	141.5	27
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Sequence 77, Appl	34	7 US-11-035-826-77	34	85.2	140.5	29
Sequence 82, Appl	34	7 US-11-035-826-82	34	85.2	140.5	30
Sequence 88, Appl	34	7 US-11-035-826-88	34	85.2	140.5	31
Sequence 100, App	34	7 US-11-035-826-100	34	85.2	140.5	32
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Sequence 271, App	34	7 US-11-035-826-271	34	85.2	140.5	36
Sequence 35, Appl	34	7 US-11-035-826-35	34	84.5	139.5	37
Sequence 39, Appl	34	7 US-11-035-826-39	34	84.5	139.5	38
Sequence 41, Appl	34	7 US-11-035-826-41	34	84.5	139.5	39
Sequence 42, Appl	34	7 US-11-035-826-42	34	84.5	139.5	40
Sequence 65, Appl	34	7 US-11-035-826-65	34	84.5	139.5	41
Sequence 79, Appl	34	7 US-11-035-826-79	34	84.5	139.5	42
Sequence 83, Appl	34	7 US-11-035-826-83	34	84.5	139.5	43
Sequence 84, Appl	34	7 US-11-035-826-84	34	84.5	139.5	44
Sequence 87, Appl	34	7 US-11-035-826-87	34	84.5	139.5	45
Sequence 94, Appl	34	7 US-11-035-826-94	34	84.5	139.5	46
Sequence 101, App	34	7 US-11-035-826-101	34	84.5	139.5	47
Sequence 103, App	34	7 US-11-035-826-103	34	84.5	139.5	48
Sequence 27, Appl	36	7 US-11-035-826-27	36	84.5	139.5	49
Sequence 40, Appl	34	7 US-11-035-826-40	34	83.9	138.5	50
Sequence 43, Appl	34	7 US-11-035-826-43	34	83.9	138.5	51
Sequence 49, Appl	34	7 US-11-035-826-49	34	83.9	138.5	52
Sequence 80, Appl	34	7 US-11-035-826-80	34	83.9	138.5	53
Sequence 91, Appl	34	7 US-11-035-826-91	34	83.9	138.5	54
Sequence 93, Appl	34	7 US-11-035-826-93	34	83.9	138.5	55
Sequence 48, Appl	34	7 US-11-035-826-48	34	83.3	137.5	56
Sequence 57, Appl	34	7 US-11-035-826-57	34	83.3	137.5	57
Sequence 58, Appl	34	7 US-11-035-826-58	34	83.3	137.5	58
Sequence 73, Appl	34	7 US-11-035-826-73	34	83.3	137.5	59
Sequence 81, Appl	34	7 US-11-035-826-81	34	83.3	137.5	60
Sequence 89, Appl	34	7 US-11-035-826-89	34	83.3	137.5	61
Sequence 102, App	34	7 US-11-035-826-102	34	83.3	137.5	62
Sequence 64, Appl	34	7 US-11-035-826-64	34	82.7	136.5	63
Sequence 188, App	34	7 US-11-035-826-188	34	82.7	136.5	64
Sequence 190, App	34	7 US-11-035-826-190	34	82.7	136.5	65
Sequence 200, App	34	7 US-11-035-826-200	34	82.7	136.5	66
Sequence 272, App	34	7 US-11-035-826-272	34	82.7	136.5	67
Sequence 24, Appl	34	7 US-11-035-826-24	34	82.1	135.5	68
Sequence 54, Appl	34	7 US-11-035-826-54	34	82.1	135.5	69
Sequence 55, Appl	34	7 US-11-035-826-55	34	82.1	135.5	70
Sequence 62, Appl	34	7 US-11-035-826-62	34	82.1	135.5	71
Sequence 86, Appl	34	7 US-11-035-826-86	34	82.1	135.5	72
Sequence 53, Appl	34	7 US-11-035-826-53	34	81.5	134.5	73
Sequence 75, Appl	34	7 US-11-035-826-75	34	81.5	134.5	74
Sequence 70, Appl	34	7 US-11-035-826-70	34	80.9	133.5	75
Sequence 92, Appl	34	7 US-11-035-826-92	34	80.9	133.5	76
Sequence 44, Appl	34	7 US-11-035-826-44	34	80.3	132.5	77
Sequence 63, Appl	34	7 US-11-035-826-63	34	80.3	132.5	78
Sequence 90, Appl	34	7 US-11-035-826-90	34	80.3	132.5	79
Sequence 184, App	34	7 US-11-035-826-184	34	80.3	132.5	80
Sequence 196, App	34	7 US-11-035-826-196	34	80.3	132.5	81
Sequence 38, Appl	34	7 US-11-035-826-38	34	79.7	131.5	82
Sequence 45, Appl	34	7 US-11-035-826-45	34	79.7	131.5	83
Sequence 51, Appl	34	7 US-11-035-826-51	34	79.7	131.5	84
Sequence 61, Appl	34	7 US-11-035-826-61	34	79.7	131.5	85
Sequence 68, Appl	34	7 US-11-035-826-68	34	79.7	131.5	86
Sequence 72, Appl	34	7 US-11-035-826-72	34	79.7	131.5	87
Sequence 194, App	34	7 US-11-035-826-194	34	79.7	131.5	88
Sequence 274, App	34	7 US-11-035-826-274	34	79.7	131.5	89
Sequence 31, Appl	36	7 US-11-035-826-31	36	79.7	131.5	90
Sequence 28, Appl	34	7 US-11-035-826-28	34	79.1	130.5	91
Sequence 36, Appl	34	7 US-11-035-826-36	34	79.1	130.5	92
Sequence 52, Appl	36	7 US-11-035-826-52	36	79.1	130.5	93
Sequence 47, Appl	34	7 US-11-035-826-47	34	78.5	129.5	94
Sequence 277, App	34	7 US-11-035-826-277	34	77.9	128.5	95
Sequence 3, Appl	31	7 US-11-126-996-3	31	77.3	127.5	96
Sequence 21, Appl	31	7 US-11-035-826-21	31	77.3	127.5	97
Sequence 269, App	31	7 US-11-035-826-269	31	77.3	127.5	98

99 127.5 77.3 34 7 US-11-176-735-18 Sequence 18, Appl
100 127.5 77.3 34 7 US-11-035-826-26 Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-11-035-826-37
; Sequence 37, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37

LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)..(7)
OTHER INFORMATION: Cha
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)..(8)
OTHER INFORMATION: Nle
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: Cha
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (18)..(18)
OTHER INFORMATION: Nle
US-11-035-826-37

Query Match 90.0%; Score 148.5; DB 7; Length 34;
Best Local Similarity 97.1%; Pred. No. 1.7e-15;
Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Oy 1 SVSEIQ-XHNKXGKHLNSXERVEWLRKKLQDVHNY 33
Db 1 SVSEIQXXHNKXGKHLNSXERVEWLRKKLQDVHNY 34

RESULT 2
US-11-035-826-192
; Sequence 192, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES

; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 192

LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)..(8)
OTHER INFORMATION: Nle
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (18)..(18)
OTHER INFORMATION: Nle
FEATURE:
OTHER INFORMATION: Disulphide or amide bond between residues 26 and 30
US-11-035-826-192

Query Match 90.0%; Score 148.5; DB 7; Length 34;
Best Local Similarity 94.1%; Pred. No. 1.7e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Oy 1 SVSEIQ-XHNKXGKHLNSXERVEWLRKKLQDVHNY 33
Db 1 SVSEIQXHNKXGKHLNSXERVEWLRKKLQDVHNY 34

RESULT 3
US-11-176-735-19
; Sequence 19, Application US/11176735
; Publication No. US20050272660A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, T.J.
; APPLICANT: Kronenberg, H.M.
; APPLICANT: Potts, J.T.
; APPLICANT: Juppner, H.
; TITLE OF INVENTION: Polypeptide Derivatives of Parathyroid Hormone (PTH)
; FILE REFERENCE: 0609.4820002
; CURRENT APPLICATION NUMBER: US/11/176,735
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: US/09/672,020
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/185,060
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: PCT/US00/04716
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 60/156,927
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-11-176-735-19

Query Match 87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 85.3%; Pred. No. 6.3e-15;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVWLRKKLQDVHNY 33
||||| || ||||| ||||| ||||| ||||| :
Db 1 SVSEIQLMNLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 4
US-11-126-996-2
; Sequence 2, Application US/11126996
; Publication No. US20050276843A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; APPLICANT: Costantino, Henry R.
; APPLICANT: Kleppe, Mary S.
; APPLICANT: Li, Ching-Yuan
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal Delivery of Parathyroid Hormone
; FILE REFERENCE: 04-04US
; CURRENT APPLICATION NUMBER: US/11/126,996
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,113
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-126-996-2

Query Match 87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 85.3%; Pred. No. 6.3e-15;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVWLRKKLQDVHNY 33
||||| || ||||| ||||| ||||| ||||| :
Db 1 SVSEIQLMNLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 5
US-11-035-826-18
; Sequence 18, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-035-826-18

Query Match 87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 85.3%; Pred. No. 6.3e-15;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVWLRKKLQDVHNY 33
||||| || ||||| ||||| ||||| ||||| :
Db 1 SVSEIQLMNLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 6
US-11-035-826-33
; Sequence 33, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD.RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Cha
US-11-035-826-33

Query Match 87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 85.3%; Pred. No. 6.3e-15;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVWLRKKLQDVHNY 33
||||| || ||||| ||||| ||||| ||||| :
Db 1 SVSEIQLMNLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 7
US-11-035-826-34
; Sequence 34, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
US-11-035-826-34

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: Cha
US-11-035-826-34

Query Match      87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 88.2%; Pred. No. 6.3e-15;
Matches 30; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSERVEWLKRLKLDVHNY 33
||||| ||||||| ||||||| ||||||| |||||||
Db 1 SVSEIQLMHNKGKHLNSERVEWLKRLKLDVHNF 34

RESULT 8
US-11-035-826-36
; Sequence 36, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; PRIOR FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Cha
US-11-035-826-36

Query Match      87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 88.2%; Pred. No. 6.3e-15;
Matches 30; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSERVEWLKRLKLDVHNY 33
||||| ||||||| ||||||| ||||||| |||||||
Db 1 SVSEIQLMHNKGKHLNSERVEWLKRLKLDVHNF 34

RESULT 9
US-11-035-826-67
; Sequence 67, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; PRIOR FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Cha
US-11-035-826-67

Query Match      87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 88.2%; Pred. No. 6.3e-15;
Matches 30; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSERVEWLKRLKLDVHNY 33
||||| ||||||| ||||||| ||||||| |||||||
Db 1 SVSEIQLMHNKGKHLNSERVEWLKRLKLDVHNF 34

RESULT 10
US-11-035-826-78
; Sequence 78, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; PRIOR FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: Cha
US-11-035-826-78

Query Match      87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 93.9%; Pred. No. 6.3e-15;
Matches 31; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 VSEIQ-XHNKGKHLNSERVEWLKRLKLDVHNY 33
||||| ||||||| ||||||| ||||||| |||||||
Db 2 VSEIQLMHNKGKHLNSERVEWLKRLKLDVHNY 34

RESULT 10
US-11-035-826-78
; Sequence 78, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; PRIOR FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78
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; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: Cha
US-11-035-826-78

Query Match      87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 88.2%; Pred. No. 6.3e-15;
Matches 30; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXRVWLKRLKLDVHNY 33
    ||||| ||| ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQXHNXGKHLNSMERVWLKRLKLDVHNF 34

RESULT 11
US-11-035-826-97
; Sequence 97, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 97
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-035-826-97

Query Match      87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 85.3%; Pred. No. 6.3e-15;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXRVWLKRLKLDVHNY 33
    ||||| ||| ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQFMENFGKHLNSMERVWLKRLKLDVHNF 34

RESULT 12
US-11-035-826-98
; Sequence 98, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
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; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Nal
; NAME/KEY: MOD RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: Nal
US-11-035-826-98

Query Match      87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 88.2%; Pred. No. 6.3e-15;
Matches 30; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXRVWLKRLKLDVHNY 33
    ||||| ||| ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQXHNXGKHLNSMERVWLKRLKLDVHNF 34

RESULT 13
US-11-035-826-186
; Sequence 186, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 186
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: Nle
; NAME/KEY: MOD RES
; LOCATION: (18)..(18)
; OTHER INFORMATION: Nle
; FEATURE:
; OTHER INFORMATION: Disulphide or amide bond between residues 13 and 17
US-11-035-826-186
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Query Match      87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 91.2%; Pred. No. 6.3e-15;
Matches 31; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSXERVWLKRLKLDVHNY 33
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQLXHNGLKHLNLSXERVWLKRLKLDVHNY 34

RESULT 14
US-11-035-826-189
; Sequence 189, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 189
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Disulphide or amide bond between residues 26 and 30
US-11-035-826-189

Query Match      87.6%; Score 144.5; DB 7; Length 34;
Best Local Similarity 88.2%; Pred. No. 6.3e-15;
Matches 30; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSXERVWLKRLKLDVHNY 33
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQLXHNGLKHLNLSXERVWLKRLKLDVHNY 34

RESULT 16
US-11-035-826-20
; Sequence 20, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-035-826-20

Query Match      87.6%; Score 144.5; DB 7; Length 36;
Best Local Similarity 85.3%; Pred. No. 6.7e-15;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSXERVWLKRLKLDVHNY 33
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQLXHNGLKHLNLSXERVWLKRLKLDVHNF 34

RESULT 15
US-11-035-826-198
; Sequence 198, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
```

```
; Sequence 19, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-035-826-19

Query Match      87.6%; Score 144.5; DB 7; Length 37;
Best Local Similarity 85.3%; Pred. No. 6.9e-15;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVEWLKRLQDVHNY 33
DB 1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34

RESULT 18
US-11-126-996-1
; Sequence 1, Application US/11126996
; Publication No. US20050276843A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; APPLICANT: Costantino, Henry R.
; APPLICANT: Kleppe, Mary S.
; APPLICANT: Li, Ching-yuan
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal Delivery of Parathyroid Hormone
; FILE REFERENCE: 04-04US
; CURRENT APPLICATION NUMBER: US/11/126,996
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,113
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-126-996-1

Query Match      87.6%; Score 144.5; DB 7; Length 84;
Best Local Similarity 85.3%; Pred. No. 1.7e-14;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVEWLKRLQDVHNY 33
DB 1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34

RESULT 19
US-11-035-826-15
```

```
; Sequence 15, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-035-826-15

Query Match      87.6%; Score 144.5; DB 7; Length 84;
Best Local Similarity 85.3%; Pred. No. 1.7e-14;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVEWLKRLQDVHNY 33
DB 1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34

RESULT 20
US-11-035-826-99
; Sequence 99, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-035-826-99

Query Match      87.0%; Score 143.5; DB 7; Length 34;
Best Local Similarity 85.3%; Pred. No. 8.8e-15;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
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Qy 1 SVSEIQ-XHNKGKHLNSXRVWLKQDVHNY 33
Db 1 SVSEIQXHNKGKHLNSXRVWLKQDVHNF 34

RESULT 21

US-11-035-826-85
; Sequence 85, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: (7)..(7)
; OTHER INFORMATION: Cha
; NAME/KEY: MOD RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: Cha
; NAME/KEY: MOD RES
; LOCATION: (18)..(18)
; OTHER INFORMATION: Nle
; NAME/KEY: MOD RES
; LOCATION: (19)..(19)
; OTHER INFORMATION: Aib
US-11-035-826-85

Query Match 86.4%; Score 142.5; DB 7; Length 34;
Best Local Similarity 94.1%; Pred. No. 1.2e-14;
Matches 32; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSXRVWLKQDVHNY 33
Db 1 SVSEIQXHNKGKHLNSXRVWLKQDVHNY 34

RESULT 22

US-11-035-826-50
; Sequence 50, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,

; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (34)..(34)
; OTHER INFORMATION: Aib
US-11-035-826-50

Query Match 85.8%; Score 141.5; DB 7; Length 34;
Best Local Similarity 87.9%; Pred. No. 1.7e-14;
Matches 29; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSXRVWLKQDVHNY 32
Db 1 SVSEIQXHNKGKHLNSXRVWLKQDVHNY 33

RESULT 23

US-11-035-826-59
; Sequence 59, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Cha
; NAME/KEY: MOD RES
; LOCATION: (34)..(34)
; OTHER INFORMATION: Aib

US-11-035-826-59

Query Match 85.8%; Score 141.5; DB 7; Length 34;
Best Local Similarity 87.9%; Pred. No. 1.7e-14;
Matches 29; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVELRKKLQDVHN 32
||||| ||||||| ||||||| ||||||| |||||||
DB 1 SVSEIQXHNKLGKHLNSMERVELRKKLQDVHN 33

RESULT 24

US-11-035-826-60
; Sequence 60, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: Cha
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (34)..(34)
; OTHER INFORMATION: Aib
US-11-035-826-60

Query Match 85.8%; Score 141.5; DB 7; Length 34;
Best Local Similarity 90.9%; Pred. No. 1.7e-14;
Matches 30; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVELRKKLQDVHN 32
||||| ||||||| ||||||| ||||||| |||||||
DB 1 SVSEIQXHNKLGKHLNSMERVELRKKLQDVHN 33

RESULT 25

US-11-035-826-66
; Sequence 66, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524

; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (27)..(27)
; OTHER INFORMATION: hArg
US-11-035-826-66

Query Match 85.8%; Score 141.5; DB 7; Length 34;
Best Local Similarity 82.4%; Pred. No. 1.7e-14;
Matches 28; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVELRKKLQDVHN 33
||||| ||||||| ||||||| ||||||| |||||||
DB 1 SVSEIQXHNKLGKHLNSMERVELRKKLQDVHN 34

RESULT 26

US-11-035-826-76
; Sequence 76, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: Cha
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: Nle
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: Cha
; FEATURE:
; NAME/KEY: MOD_RES

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; LOCATION: (18)..(18)
; OTHER INFORMATION: Nle
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (34)..(34)
; OTHER INFORMATION: Aib
US-11-035-826-76

Query Match      85.8%; Score 141.5; DB 7; Length 34;
Best Local Similarity 97.0%; Pred. No. 1.7e-14;
Matches 32; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKXGHLNSXRVWLRKQLQDVHN 32
Db 1 SVSEIQXHNKXGHLNSXRVWLRKQLQDVHN 33

RESULT 27
US-11-035-826-260
; Sequence 260, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 260
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: Met, Ala, Ser, Val, Leu, Ile, or Trp
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (18)..(18)
; OTHER INFORMATION: Met, Ala, Ser, Val, Leu, Ile, or Trp
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (34)..(34)
; OTHER INFORMATION: Phe or Tyr
; OTHER INFORMATION: See specification as filed for detailed description of
; OTHER INFORMATION: substitutions and preferred embodiments
US-11-035-826-279

Query Match      85.8%; Score 141.5; DB 7; Length 34;
Best Local Similarity 93.9%; Pred. No. 1.7e-14;
Matches 31; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKXGHLNSXRVWLRKQLQDVHN 32
Db 1 SVSEIQXHNKXGHLNSXRVWLRKQLQDVHN 33

RESULT 29
US-11-035-826-77
; Sequence 77, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)..(3)
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; OTHER INFORMATION: Aib
US-11-035-826-77

Query Match      85.2%; Score 140.5; DB 7; Length 34;
Best Local Similarity 82.4%; Pred. No. 2.4e-14;
Matches 28; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVWLKRLQDVHNY 33
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQLMHNLGKHLNSMERVWLKRLQDVHNF 34

RESULT 30
US-11-035-826-82
; Sequence 82, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 82
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (17)..(17)
; OTHER INFORMATION: Aib
US-11-035-826-82

Query Match      85.2%; Score 140.5; DB 7; Length 34;
Best Local Similarity 82.4%; Pred. No. 2.4e-14;
Matches 28; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVWLKRLQDVHNY 33
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQLMHNLGKHLNSMERVWLKRLQDVHNF 34

RESULT 31
US-11-035-826-88
; Sequence 88, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
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; OTHER INFORMATION: Aib
US-11-035-826-77

Query Match      85.2%; Score 140.5; DB 7; Length 34;
Best Local Similarity 82.4%; Pred. No. 2.4e-14;
Matches 28; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVWLKRLQDVHNY 33
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQLMHNLGKHLNSMERVWLKRLQDVHNF 34

RESULT 32
US-11-035-826-100
; Sequence 100, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 100
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-035-826-100

Query Match      85.2%; Score 140.5; DB 7; Length 34;
Best Local Similarity 82.4%; Pred. No. 2.4e-14;
Matches 28; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVWLKRLQDVHNY 33
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 SVSEIQFMHNFGRHNSMERVWLKRLQDVHNF 34

RESULT 33
US-11-035-826-183
; Sequence 183, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
```

APPLICANT: HOLST, JENS JUUL
TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
FILE REFERENCE: 57736 CIP2(46865)
CURRENT APPLICATION NUMBER: US/11/035,826
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 10/393,524
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: 09/954,304
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: GB 0022844.5
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: GB 0029920.6
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/371,307
PRIOR FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 279
SOFTWARE: PatentIn version 3.3
SEQ ID NO 183
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Disulphide or amide bond between residues 13 and 17
US-11-035-826-193

Query Match 85.2%; Score 140.5; DB 7; Length 34;
Best Local Similarity 82.4%; Pred. No. 2.4e-14;
Matches 28; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKXGHLNSXRVWLKRLKQDVHNY 33
Db 1 SVSEIQLMHNKGLNDMVERWLKRLKQDVHNF 34

RESULT 34
US-11-035-826-193
Sequence 193, Application US/11035826
Publication No. US20050282749A1
GENERAL INFORMATION:
APPLICANT: HOLST, JENS JUUL
TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
FILE REFERENCE: 57736 CIP2(46865)
CURRENT APPLICATION NUMBER: US/11/035,826
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 10/393,524
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: 09/954,304
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: GB 0022844.5
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: GB 0029920.6
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/371,307
PRIOR FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 279
SOFTWARE: PatentIn version 3.3
SEQ ID NO 193
LENGTH: 34
TYPE: PRT
ORGANISM: Bos sp.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)..(8)
OTHER INFORMATION: N1e
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (18)..(18)
OTHER INFORMATION: N1e

FEATURE:
OTHER INFORMATION: Disulphide or amide bond between residues 26 and 30
US-11-035-826-193

Query Match 85.2%; Score 140.5; DB 7; Length 34;
Best Local Similarity 88.2%; Pred. No. 2.4e-14;
Matches 30; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKXGHLNSXRVWLKRLKQDVHNY 33
Db 1 AVSEIQFXHNLGHLSSXRVWLKRLKQDVHNY 34

RESULT 35
US-11-035-826-195
Sequence 195, Application US/11035826
Publication No. US20050282749A1
GENERAL INFORMATION:
APPLICANT: HENRIKSEN, DENNIS BANG
APPLICANT: HOLST, JENS JUUL
TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
FILE REFERENCE: 57736 CIP2(46865)
CURRENT APPLICATION NUMBER: US/11/035,826
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 10/393,524
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: 09/954,304
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: GB 0022844.5
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: GB 0029920.6
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/371,307
PRIOR FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 279
SOFTWARE: PatentIn version 3.3
SEQ ID NO 195
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Disulphide or amide bond between residues 13 and 17
FEATURE:
OTHER INFORMATION: Disulphide or amide bond between residues 26 and 30
US-11-035-826-195

Query Match 85.2%; Score 140.5; DB 7; Length 34;
Best Local Similarity 82.4%; Pred. No. 2.4e-14;
Matches 28; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKXGHLNSXRVWLKRLKQDVHNY 33
Db 1 SVSEIQLMHNKGLNDMVERWLKRLKQDVHNF 34

RESULT 36
US-11-035-826-271
Sequence 271, Application US/11035826
Publication No. US20050282749A1
GENERAL INFORMATION:
APPLICANT: HENRIKSEN, DENNIS BANG
APPLICANT: HOLST, JENS JUUL
TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
FILE REFERENCE: 57736 CIP2(46865)
CURRENT APPLICATION NUMBER: US/11/035,826
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 10/393,524
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: 09/954,304

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; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 271
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Gly, D-Ser, D-Ala, or Tyr
US-11-035-826-271

Query Match      85.2%; Score 140.5; DB 7; Length 34;
Best Local Similarity 84.8%; Pred. No. 2.4e-14;
Matches 28; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY      2 VSEIQ-XHNKXGHLNSXERVEWLKRLQDVHNY 33
      ||||| || ||||| ||||| ||||| ||||| |||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34

RESULT 37
US-11-035-826-35
; Sequence 35, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (15)..(15)
; OTHER INFORMATION: Cha
US-11-035-826-35

Query Match      84.5%; Score 139.5; DB 7; Length 34;
Best Local Similarity 82.4%; Pred. No. 3.3e-14;
Matches 28; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY      1 SVSEIQ-XHNKXGHLNSXERVEWLKRLQDVHNY 33
      ||||| || ||||| ||||| ||||| ||||| |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34

RESULT 39
US-11-035-826-41
; Sequence 41, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (15)..(15)
; OTHER INFORMATION: Cha
US-11-035-826-41

Query Match      84.5%; Score 139.5; DB 7; Length 34;
Best Local Similarity 82.4%; Pred. No. 3.3e-14;
Matches 28; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY      1 SVSEIQ-XHNKXGHLNSXERVEWLKRLQDVHNY 33
      ||||| || ||||| ||||| ||||| ||||| |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLKRLQDVHNF 34

RESULT 39
US-11-035-826-41
; Sequence 41, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (15)..(15)
; OTHER INFORMATION: Cha
US-11-035-826-41
```

; NAME/KEY: MOD RES
; LOCATION: (26)..(28)
; OTHER INFORMATION: Cha
US-11-035-826-41

Query Match 84.5%; Score 139.5; DB 7; Length 34;
Best Local Similarity 82.4%; Pred. No. 3.3e-14;
Matches 28; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGHLNSXERVEWLKKLQDVHNY 33
||||| |||||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLKKKQDVHNF 34
||||| |||||||

RESULT 40

US-11-035-826-42
; Sequence 42, Application US/11035826
; Publication No. US20050282749A1
; GENERAL INFORMATION:
; APPLICANT: HENRIKSEN, DENNIS BANG
; APPLICANT: HOLST, JENS JUUL
; TITLE OF INVENTION: USE OF GLP-2 AND RELATED COMPOUNDS FOR THE TREATMENT,
; TITLE OF INVENTION: PREVENTION, DIAGNOSIS, AND PROGNOSIS OF BONE-RELATED
; TITLE OF INVENTION: DISORDERS AND CALCIUM HOMEOSTASIS RELATED SYNDROMES
; FILE REFERENCE: 57736 CIP2(46865)
; CURRENT APPLICATION NUMBER: US/11/035,826
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 10/393,524
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 09/954,304
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: GB 0022844.5
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 0029920.6
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/371,307
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 279
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (31)..(31)
; OTHER INFORMATION: Cha
US-11-035-826-42

Query Match 84.5%; Score 139.5; DB 7; Length 34;
Best Local Similarity 82.4%; Pred. No. 3.3e-14;
Matches 28; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGHLNSXERVEWLKKLQDVHNY 33
||||| |||||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLKKKQDVHNF 34
||||| |||||||

Search completed: January 28, 2006, 01:38:26
Job time : 9 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2006, 01:07:47 ; Search time 38 Seconds
(without alignments)
83.557 Million cell updates/sec

Title: US-09-674-597A-16

Perfect score: 165

Sequence: 1 SVSEIQHXNGKHLNSXRVEMLRKKLQDVHNY 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	144.5	87.6	115	1	PTHU
2	139.5	84.5	115	1	PTPG
3	139.5	84.5	115	2	JC4202
4	136.5	82.7	115	1	PTBO
5	127.5	77.3	115	2	A05091
6	119.5	72.4	105	2	I51851
7	96.5	58.5	119	2	A34937
8	59	35.8	1257	1	I58383
9	59	35.8	3678	2	S28916
10	55	33.3	764	1	BBHU
11	52.5	31.8	1172	2	T00065
12	52	31.5	3685	1	A27605
13	51	30.9	118	2	T44470
14	51	30.9	240	1	TQEC34
15	51	30.9	236	2	S09261
16	51	30.9	2479	1	MNVRA
17	50	30.3	334	2	F86462
18	50	30.3	513	1	RGECAV
19	50	30.3	513	2	F90866
20	50	30.3	513	2	C85752
21	50	30.3	838	2	C84854
22	49.5	30.0	2364	1	A44159
23	49	29.7	94	2	T09450
24	49	29.7	94	2	C64559
25	49	29.7	948	2	S26945
26	49	29.7	2024	2	A54103
27	48.5	29.4	1354	2	S74244
28	48	29.1	162	2	T10831
29	48	29.1	229	2	E85806

30	48	29.1	229	2	D90958	hypothetical prote
31	48	29.1	286	2	B69834	conserved hypotet
32	48	29.1	295	2	F90938	hypothetical prote
33	48	29.1	295	2	B85664	transposase for IS
34	48	29.1	295	2	D90801	hypothetical prote
35	48	29.1	295	2	B85613	probable transposa
36	48	29.1	295	2	B85787	probable transposa
37	48	29.1	295	2	T00315	transposase - Esch
38	48	29.1	295	2	E85661	probable transposa
39	48	29.1	299	2	T05866	hypothetical prote
40	48	29.1	687	2	E69733	PBSX prophage ORF
41	48	29.1	1038	2	T15098	hypothetical prote
42	48	29.1	1295	2	T30528	reverse transcript
43	47.5	28.8	189	2	T19559	hypothetical prote
44	47.5	28.8	462	1	S00552	mitochondrial proc
45	47	28.5	312	2	T33296	hypothetical prote
46	47	28.5	326	2	H97346	oligopeptide ABC t
47	47	28.5	403	2	T09634	phosphoglycerate k
48	47	28.5	752	1	C2HU	complement C2 prec
49	46.5	28.2	167	2	AC0481	probable gluconoki
50	46.5	28.2	168	2	S36294	T-cell receptor ga
51	46.5	28.2	178	2	AB0310	gluconokinase (EC
52	46.5	28.2	179	2	S36289	T-cell receptor ga
53	46.5	28.2	202	2	S36293	hydrolase (importe
54	46.5	28.2	286	2	AG3220	probable transpos
55	46.5	28.2	346	2	H85057	hypothetical prote
56	46	27.9	138	2	T49183	ribosomal protein
57	46	27.9	183	1	R58Y32	transposase for IS
58	46	27.9	296	2	A85698	transposase for IS
59	46	27.9	296	2	A99840	transposase for IS
60	46	27.9	296	2	C90978	IS629 transposase
61	46	27.9	296	2	H85824	probable RNA helic
62	46	27.9	506	1	S31229	leucine-tRNA ligas
63	46	27.9	924	2	F72408	hypothetical prote
64	46	27.9	947	2	T08605	hypothetical prote
65	46	27.9	1189	1	JC2366	protein-tyrosine-p
66	46	27.9	1232	2	A48446	DNA topoisomerase
67	46	27.9	1422	2	T18404	chromatin remodel
68	46	27.9	2109	2	I38414	transcription fact
69	46	27.9	3131	2	S39842	enmiatin synthetas
70	46	27.9	3660	1	S02041	dystrophin, muscle
71	45.5	27.6	90	2	A97755	hypothetical prote
72	45.5	27.6	136	2	G82240	hypothetical prote
73	45.5	27.6	206	2	C49054	T-cell receptor ga
74	45.5	27.6	278	2	T24330	hypothetical prote
75	45.5	27.6	348	2	B75097	hypothetical prote
76	45.5	27.6	353	2	A70365	conserved hypotet
77	45.5	27.6	385	2	AE3402	ribonuclease III (
78	45.5	27.6	564	1	HMITVC2	hemagglutinin prec
79	45.5	27.6	653	2	H96630	hypothetical prote
80	45.5	27.6	762	2	G66999	hydrogenase matura
81	45.5	27.6	837	2	H82970	hypothetical prote
82	45.5	27.6	1082	2	H70360	cation efflux syst
83	45.5	27.6	1354	2	S69211	serine/threonine-s
84	45.5	27.6	1387	2	T30335	KLP2 protein - Afr
85	45	27.3	187	2	S70186	21K protein - Shig
86	45	27.3	201	2	G71428	hypothetical prote
87	45	27.3	319	2	T45980	hypothetical prote
88	45	27.3	323	2	F84423	hypothetical prote
89	45	27.3	330	2	T45981	hypothetical prote
90	45	27.3	356	2	T04665	probable serine/th
91	45	27.3	415	2	C85420	protein kinase-lik
92	45	27.3	421	2	D97207	phospholipase C fa
93	45	27.3	441	2	B84854	hypothetical prote
94	45	27.3	445	2	JQ0422	beta-tubulin 1 - a
95	45	27.3	471	2	T21349	hypothetical prote
96	45	27.3	531	1	T51956	probable beta-gluc
97	45	27.3	594	1	E64622	excinuclease ABC c
98	45	27.3	594	2	B71893	excinuclease ABC c
99	45	27.3	924	2	S34926	hypothetical prote
100	45	27.3	1043	2	T13172	gag-like protein p

A;Residues: 1-115 <SCH>
A;Cross-references: UNIPROT:P01269; UNIPARC:UPI0000132908; GB:X05722; GB:Y00409; NID:glb
R;Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
Biochemistry 14, 3631-3635, 1975
A;Title: Porcine parathyroid hormone. Identification, biosynthesis, and partial amino
A;Reference number: A90390; MUID:76018954; PMID:1164500
A;Accession: A90390
A;Molecule type: protein
A;Residues: 26-115 <CHU>
A;Cross-references: UNIPARC:UPI00001592DF
R;Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., J.
Biochemistry 13, 1994-1999, 1974
A;Title: The amino acid sequence of porcine parathyroid hormone.
A;Reference number: A90376; MUID:7425317; PMID:4840833
A;Accession: A90376
A;Molecule type: protein
A;Residues: 32-109 <SAU>
A;Cross-references: UNIPARC:UPI00001734E0
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Accession: A90030
A;Molecule type: protein
A;Residues: 32-115 <KRO>
A;Cross-references: UNIPARC:UPI0000132907; GB:V00106; GB:J00023; NID:984; PIDN:CAA23439
A;Note: the authors translated the codon GAA for residue 50 as Gly
R;Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D.V.
Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974
A;Title: The N-terminal amino-acid sequence of bovine parathyroid hormone I.
A;Reference number: A91648; MUID:71076162; PMID:5531031
A;Accession: A91648
A;Molecule type: protein
A;Residues: 32-115 <NIA>
A;Cross-references: UNIPARC:UPI00000473E4
R;Brewer Jr., H.B.; Ronan, R.
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970
A;Title: Bovine parathyroid hormone: amino acid sequence.
A;Reference number: A93773; MUID:71063634; PMID:5275384
A;Accession: A93773
A;Molecule type: protein
A;Residues: 32-115 <BRE>
A;Cross-references: UNIPARC:UPI00000473E4
R;Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.;
Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971
A;Title: Synthesis of a biologically active N-terminal tetraoctapeptide of parathy-
A;Reference number: A93776; MUID:71091588; PMID:4322265
A;Contents: annotation; synthesis of residues 32-65
A;Note: the synthetic peptide was active in vivo and in vitro
R;Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A;Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormo
A;Reference number: A90030; MUID:74173303; PMID:4598526
A;Accession: A90030
A;Molecule type: protein
A;Residues: 32-115 <WEA>
A;Cross-references: UNIPARC:UPI0000132907; GB:J00024; NID:gi63642; PIDN:AAA30747.1; PID
R;Weaver, C.A.; Gordon, D.F.
Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981
A;Title: introduction by molecular cloning of artifactual inverted sequences at the 5'
A;Reference number: I45975; MUID:82037785; PMID:6170060
A;Accession: I45975
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WEA>
A;Cross-references: UNIPARC:UPI0000132907; GB:J00024; NID:gi63642; PIDN:AAA30747.1; PID
R;Weaver, C.A.; Gordon, D.F.
Mol. Cell. Endocrinol. 28, 411-424, 1982
A;Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
A;Reference number: I45976; MUID:83105964; PMID:6185374
A;Accession: I45976
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-115 <WE3>
A;Cross-references: UNIPARC:UPI0000132907; GB:M25082; NID:gi63644; PIDN:AAA30748.1; PID
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A;Gene: PTH

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Best Local Similarity 82.4%; Pred. No. 6.4e-12;
Matches 28; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKXGHLNSXERVEWLKQLQDVHNY 33
Db 32 SVSEIQMHNLGKHLSSLRVEWLKQLQDVHNF 65

RESULT 3
JC4202
parathyroid hormone precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C;Accession: JC4202
R;Rosol, T.J.; Steimeyer, C.L.; McCauley, L.K.; Groene, A.; Dewille, J.W.; Capen, C.C.
Gene 160, 241-243, 1995
A;Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein and
A;Reference number: JC4201; MUID:95369696; PMID:7642102
A;Accession: JC4202
A;Molecule type: mRNA
A;Residues: 1-115 <ROS>
A;Cross-references: UNIPROT:P52212; UNIPARC:UPI0000132908; GB:U15662; NID:g558915; PIDN:
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-31/Domain: signal sequence #status predicted <SIG>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status predicted <MAT>

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Best Local Similarity 82.4%; Pred. No. 6.4e-12;
Matches 28; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKXGHLNSXERVEWLKQLQDVHNY 33
Db 32 SVSEIQFMHNLGKHLSSLRVEWLKQLQDVHNF 65

RESULT 4
PTB0
parathyroid hormone precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

A;Residues: 338-384, 'V', 386-617, 'R', 619-652, 'V', 654-778, 'T', 780-1257 <OTI>
A;Cross-references: UNIPARC:UPI000016B3C4; GB:S57153; NID:g298681; PIDN:AAB25833.1; PID:
A;Accession: I78883
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 338-384, 'V', 386-617, 'R', 619-652, 'V', 654-778, 'T', 780-1120, 1175-1257 <OTI2>
A;Cross-references: UNIPARC:UPI000016B3C5; GB:S57160; NID:g298683; PIDN:AAB25834.1; PID:
R;DeFeo-Jones, D.; Huang, P.S.; Jones, R.E.; Haskell, K.M.; Vuocolo, G.A.; Hanobik, M.G.
Nature 352, 251-254, 1991
A;Title: Cloning of cDNAs for cellular proteins that bind to the retinoblastoma gene pro
A;Reference number: S16953; MUID:91312450; PMID:1857421
A;Accession: S16953
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 855-1177, 'S', 1179-1195, 'SENIICL' <DEF>
A;Cross-references: UNIPARC:UPI00001740DD
R;Kaelin Jr., W.G.; Krek, W.; Sellers, W.R.; DeCaprio, J.A.; Ajchenbaum, F.; Fuchs, C.S.
Cell 70, 351-364, 1992
A;Title: Expression cloning of a cDNA encoding a retinoblastoma-binding protein with B2F
A;Reference number: A42997; MUID:92346721; PMID:1638635
A;Accession: B42997
A;Molecule type: mRNA
A;Residues: 'MTMTKL', 510-617, 'R', 619-1257 <KAE>
A;Cross-references: UNIPARC:UPI00001740DE
A;Experimental source: Akata cells
A;Note: the cited GenBank accession number, M96577, is apparently a misprint and does not
A;Note: sequence extracted from NCBI backbone (NCBIN:110020, NCBIP:110022)
C;Genetics:
A;Gene: GDB:RAP1
A;Cross-references: GDB:120340; OMIM:180260
A;Map position: 3q21-3q22
C;Superfamily: human retinoblastoma binding protein 1
C;Keywords: alternative splicing
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QY 13 HLNSXRVWLKQLQDVHNY 33
Db 1179 NMNSTERISFLQEKLOEKIRY 1199
RESULT 9
S28916
dystrophin - mouse
N;Alternate names: duchenne muscular dystrophy protein
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S28916; B27162; S10922; C43837; B40134
R;Bies, R.D.; Phelps, S.F.; Cortez, M.D.; Roberts, R.; Caskey, C.T.; Chamberlain, J.S.
Nucleic Acids Res. 20, 1725-1731, 1992
A;Title: Human and murine dystrophin mRNA transcripts are differentially expressed durin
A;Reference number: S28916; MUID:92253376; PMID:1579466
A;Accession: S28916
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-3678 <BIB>
A;Cross-references: UNIPROT:P11531; UNIPARC:UPI00000279E7; EMBL:M68859
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
R;Koenig, M.; Hoffman, E.P.; Bertelson, C.J.; Monaco, A.P.; Feener, C.; Kunkel, L.M.
Cell 50, 509-517, 1987
A;Title: Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary
A;Reference number: A90897; MUID:87273512; PMID:3607877
A;Accession: B27162
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-201 <KOE>
A;Cross-references: UNIPARC:UPI000017686
R;Nudel, U.; Zuk, D.; Binat, P.; Zeelon, E.; Levy, Z.; Neuman, S.; Yaffe, D.
Nature 337, 76-78, 1989

A;Title: Duchenne muscular dystrophy gene product is not identical in muscle and brain.
A;Reference number: S06461; MUID:89082658; PMID:2909892
A;Accession: S10922
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-106 <NUD>
A;Cross-references: UNIPARC:UPI0000177687; EMBL:X14183
R;Rapaport, D.; Lederfein, D.; den Dunnen, J.T.; Grootsholten, P.M.; Van Ommen, G.J.;
Differentiation 49, 187-193, 1992
A;Title: Characterization and cell type distribution of a novel, major transcript of th
A;Reference number: A43837; MUID:92316332; PMID:1377655
A;Accession: C43837
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'MRHLKG', 3069-3181 <RAP>
A;Cross-references: UNIPARC:UPI0000177688
A;Note: sequence extracted from NCBI backbone
R;Hofman, E.P.; Monaco, A.P.; Feener, C.C.; Kunkel, L.M.
Science 238, 347-350, 1987
A;Title: Conservation of the Duchenne muscular dystrophy gene in mice and humans.
A;Reference number: A40134; MUID:88018015; PMID:3659917
A;Accession: B40134
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 300-676, 'F', 678-1390 <HOF>
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A;Introns: 11/1
A;Note: the list of introns may be incomplete
C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystro
C;Keywords: actin binding; alternative splicing
F:14-233/Domain: alpha-actinin actin-binding domain homology <ACT>
F:340-449/Domain: spectrin/dystrophin repeat homology <SP1>
F:450-558/Domain: spectrin/dystrophin repeat homology <SP2>
F:2797-2924/Domain: spectrin/dystrophin repeat homology <SP3>
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Best Local Similarity 40.6%; Pred. No. 19;
Matches 13; Conservative 7; Mismatches 10; Indels 2; Gaps 1;
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Db 1425 SLEENKKNQGDANQVLSQIDVAQKQLQDV 1456
RESULT 10
BBHU
complement factor B precursor [validated] - human
N;Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; heat
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragment
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1984 #sequence revision 05-Aug-1994 #text change 09-Jul-2004
C;Accession: S34075; A44622; A09934; A19188; A19947; B19947; B25971; S14339; A44628; I5:
R;Mejia, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G.
submitted to the EMBL Data Library, March 1993
A;Reference number: S34075
A;Accession: S34075
A;Molecule type: mRNA
A;Residues: 1-764 <MEJ>
A;Cross-references: UNIPROT:P00751; UNIPARC:UPI000000D7F8; EMBL:X72875; NID:g297568; PTI
R;Woods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberg, G.; Colten, H.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A;Title: Isolation of cDNA clones for the human complement protein factor B, a class II:
A;Reference number: A44622; MUID:83039428; PMID:6957884
A;Accession: A44622
A;Molecule type: mRNA
A;Residues: 467-546; 550-595; 752-764 <WOO>
A;Cross-references: UNIPARC:UPI0000172BBD; UNIPARC:UPI0000172BBE; UNIPARC:UPI0000172BBF
A;Note: the authors translated the codon TAC at 519 as thr; the nucleic acid translatio
R;Mole, J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.
J. Biol. Chem. 259, 3407-3412, 1984
A;Title: Complete primary structure for the zymogen of human complement factor B.

A:Reference number: A20751; MUID:84161997; PMID:6546754
A:Accession: A00934
A:Molecule type: protein; mRNA
A:Residues: 26-764 <MOL>
A:Cross-references: UNIPARC:UPI0000172BC0; GB:K01566
A>Note: nucleic acid translation differs from the sequence shown in having 300-Leu, 328-Ar
A>Note: glycosylation sites were determined
R:Christie, D.L.; Gagnon, J.
Biochem. J. 209, 61-70, 1983
A>Title: Amino acid sequence of the Bb fragment from complement factor B. Sequence of the
A:Reference number: A19188; MUID:83204002; PMID:6342610
A:Contents: the final paper in a series documenting the sequence, glycosylation site, an
A:Accession: A19188
A:Molecule type: protein
A:Residues: 260-296, 'T', 298-764 <CHR>
A:Cross-references: UNIPARC:UPI0000172BC1
R:Campbell, R.D.; Porter, R.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983
A>Title: Molecular cloning and characterization of the gene coding for human complement
A:Reference number: A19947; MUID:83273641; PMID:6308626
A:Accession: A19947
A:Molecule type: DNA
A:Residues: 346-764 <CAM>
A:Cross-references: UNIPARC:UPI0000172BC2; GB:J00125
A:Accession: B19947
A:Molecule type: mRNA
A:Residues: 339-509 <CA1>
A:Cross-references: UNIPARC:UPI000016AD42; GB:J00126; NID:g1877723; PIDN:AAA36226.1; PID:
R:Wu, L.; Morley, B.J.; Campbell, R.D.
Cell 48, 331-342, 1987
A>Title: Cell-specific expression of the human complement protein factor B gene: evidence
A:Reference number: A25971; MUID:87102880; PMID:3643061
A:Accession: B25971
A:Molecule type: DNA
A:Residues: 1-99 <WUL>
A:Cross-references: UNIPARC:UPI000016AD40; GB:M15082; NID:g187699; PIDN:AAA59625.1; PID:
R:Niemann, M.A.; Shown, A.S.; Miller, E.J.
Biochem. J. 274, 473-480, 1991
A>Title: The principal site of glycation of human complement Factor B.
A:Reference number: S14339; MUID:91174758; PMID:2006911
A:Accession: S14339
A:Molecule type: protein
A:Residues: 270-329 <NIE>
A:Cross-references: UNIPARC:UPI0000172BC3
A>Note: binding site for carbohydrate to lysine under artificial conditions
R:Morley, B.J.; Campbell, R.D.
EMBO J. 3, 153-157, 1984
A>Title: Internal homologies of the Ba fragment from human complement component factor B H
A:Reference number: A4628; MUID:84158524; PMID:6323161
A:Accession: A4628
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 16-225, 'F', 227-259 <MOR>
A:Cross-references: UNIPARC:UPI0000172BC4
R:Schauble, W.; Lutrig, B.; Sokolowski, T.; Estaller, C.; Weisse, E.H.; Meyer zum Busche
Immunobiology 188, 221-232, 1993
A>Title: Human complement factor B: functional properties of a recombinant zymogen of th
A:Reference number: I54409; MUID:94041399; PMID:8225386
A:Accession: I54409
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-764 <RES>
A:Cross-references: UNIPARC:UPI000000D7F8; GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:
R:Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, S.; Volanakis, J.E.
Mol. Immunol. 30, 1587-1592, 1993
A>Title: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic conv
A:Reference number: I57824; MUID:94067177; PMID:8247029
A:Accession: I57824
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-31, 'Q', 33-764 <RE2>
A:Cross-references: UNIPARC:UPI000013E5B0; GB:I15702; NID:g291921; PIDN:AAAI6820.1; PID:

[illegible]

A;Cross-references: UNIPARC:UPI000016A859; UNIPARC:UPI000016A861; EMBL:X15148
C;Comment: Dystrophin is proposed to play a role in anchoring the cytoskeleton to the pl
C;Genetics: Defects in dystrophin are responsible for the Duchenne/Becker muscular dystro
A;Gene: GDB:DMD
A;Cross-references: GDB:119850; OMIM:310200
A;Map position: Xp21.2-Xp21.2
A;Introns: 11/1; 31/3; 62/3; 88/3; 119/3; 177/2; 217/1; 277/3; 320/3; 383/3; 444/2; 494/
3; 3055/1; 3075/2; 3096/1; 3121/1; 3188/2; 3217/1; 3269/3; 3325/2; 3362/3; 3408/2; 3421/
A;Note: the list of introns is incomplete
C;Superfamily: alpha-actinin actin-binding domain homology; spectrin/dystrophin repeat h
C;Keywords: actin binding; alternative splicing; calmodulin binding; cytoskeleton; leuc
elix
F;14-233/Domain: alpha-actinin actin-binding domain homology <ACT>
F;253-327/Region: hinge
F;338-447/Domain: spectrin/dystrophin repeat homology <SP01>
F;448-556/Domain: spectrin/dystrophin repeat homology <SP02>
F;558-667/Domain: spectrin/dystrophin repeat homology <SP03>
F;668-717/Region: hinge
F;718-828/Domain: spectrin/dystrophin repeat homology <SP04>
F;836-934/Domain: spectrin/dystrophin repeat homology <SP05>
F;938-1045/Domain: spectrin/dystrophin repeat homology <SP06>
F;1047-1154/Domain: spectrin/dystrophin repeat homology <SP07>
F;1156-1263/Domain: spectrin/dystrophin repeat homology <SP08>
F;1265-1367/Domain: spectrin/dystrophin repeat homology <SP09>
F;1372-1477/Domain: spectrin/dystrophin repeat homology <SP10>
F;1478-1568/Domain: spectrin/dystrophin repeat homology #status atypical <SP11>
F;1570-1676/Domain: spectrin/dystrophin repeat homology <SP12>
F;1678-1782/Domain: spectrin/dystrophin repeat homology <SP13>
F;1784-1875/Domain: spectrin/dystrophin repeat homology <SP14>
F;1876-1982/Domain: spectrin/dystrophin repeat homology <SP15>
F;1984-2101/Domain: spectrin/dystrophin repeat homology <SP16>
F;2103-2208/Domain: spectrin/dystrophin repeat homology <SP17>
F;2210-2316/Domain: spectrin/dystrophin repeat homology <SP18>
F;2327-2423/Domain: spectrin/dystrophin repeat homology <SP19>
F;2424-2470/Region: hinge
F;2471-2577/Domain: spectrin/dystrophin repeat homology <SP20>
F;2579-2686/Domain: spectrin/dystrophin repeat homology <SP21>
F;2688-2802/Domain: spectrin/dystrophin repeat homology <SP22>
F;2804-2931/Domain: spectrin/dystrophin repeat homology <SP23>
F;2933-3040/Domain: spectrin/dystrophin repeat homology <SP24>
F;3041-3112/Region: hinge
F;3055-3092/Domain: WW repeat homology <WW1>
F;3080-3360/Region: cysteine-rich
F;3506-3527/Region: leucine zipper motif
F;3572-3593/Region: leucine zipper motif
Query Match 31.5%; Score 52; DB 1; Length 3685;
Best Local Similarity 37.5%; Pred. No. 1.7e+02;
Matches 12; Conservative 7; Mismatches 11; Indels 2; Gaps 1;
QY 1 SVSEIQXNKGKHL-NSXRVWLKQLQDV 30
DB 1423 SLSEMKKNGKGAQRVLSDVAQKQLQDV 1454
RESULT 13
T44470
Transposase tnpD [imported] - Shigella flexneri
C;Species: Shigella flexneri
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44470
R;Moss, J.E.; Cardozo, T.J.; Zychlinsky, A.; Groisman, E.A.
Mol. Microbiol. 33, 74-83, 1999
A;Title: The selC-associated SHI-2 pathogenicity island of Shigella flexneri.
A;Reference number: Z22779; MUID:99340540; PMID:10411725
A;Accession: T44470
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-118 <MOS>
A;Cross-references: UNIPROT:Q9XC10; UNIPARC:UPI00000BA934; EMBL:AF141323; NID:g5532445;
A;Experimental source: strain M90T; serotype 5a
C;Genetics:

A;Gene: tnpD

Query Match 30.9%; Score 51; DB 2; Length 118;
Best Local Similarity 33.3%; Pred. No. 7.5;
Matches 9; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 6 QXHNKXGHLNSXRVWLKQLQDVHN 32

DB 34 QRHPDKRSARAQRDDLKKEIQRYVD 60

RESULT 14

TQEC34

transposase - Escherichia coli insertion sequence IS3411

C;Species: Escherichia coli

C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004

C;Accession: A27744

R;ishiguro, N.; Sato, G.

J. Bacteriol. 170, 1902-1906, 1988

A;Title: Nucleotide sequence of insertion sequence IS3411, which flanks the citrate util
A;Reference number: A27744; MUID:88169522; PMID:2832386

A;Accession: A27744

A;Molecule type: DNA

A;Residues: 1-240 <ISH>

A;Cross-references: UNIPROT:P11257; UNIPARC:UPI000013682C; GB:M19532; NID:g154871; PIDN

A;Experimental source: strain K12

C;Genetics:

A;Mobile element: insertion sequence IS

C;Superfamily: transposase IS3

C;Keywords: DNA binding; DNA replication

Query Match 30.9%; Score 51; DB 1; Length 240;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 9; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 6 QXHNKXGHLNSXRVWLKQLQDVHN 32

DB 34 QRHPDKRSARAQRDDLKKEIQRYVD 60

RESULT 15

S09261

Probable transposase B - Shigella sonnei insertion sequence IS629

C;Species: Shigella sonnei

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004

C;Accession: S09261; S03414

R;Matsutani, S.; Ohtsubo, E.

Nucleic Acids Res. 18, 1899, 1990

A;Title: Complete sequence of IS629.

A;Reference number: S09260; MUID:90245593; PMID:2159625

A;Accession: S09261

A;Molecule type: DNA

A;Residues: 1-296 <MAT>

A;Cross-references: UNIPROT:P16942; UNIPARC:UPI0000136842; EMBL:X51586; NID:g47538; PIDN

R;Matsutani, S.; Ohtsubo, H.; Maeda, Y.; Ohtsubo, E.

J. Mol. Biol. 196, 445-455, 1987

A;Title: Isolation and characterization of IS elements repeated in the bacterial chromos
A;Reference number: S03411; MUID:88062685; PMID:2824781

A;Accession: S03414

A;Molecule type: DNA

A;Residues: 2-26;208-296 <MAY>

A;Cross-references: UNIPARC:UPI000017834C; UNIPARC:UPI000017834D; EMBL:X05953

C;Genetics:

A;Mobile element: insertion sequence IS629

C;Superfamily: transposase IS3

C;Keywords: DNA binding

Query Match 30.9%; Score 51; DB 2; Length 296;
Best Local Similarity 33.3%; Pred. No. 19;
Matches 9; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 6 QXHNKXGHLNSXRVWLKQLQDVHN 32

DB 34 QRHPDKRSARAQRDDLKKEIQRYVD 60

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: C64559
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-94 <TM>
A:Cross-references: UNIPROT:O05728; UNIPARC:UPI0000138112; GB:A5000549; GB:A5000511; NID:
C:Superfamily: virulence-associated protein vapD

Query Match 29.7%; Score 49; DB 2; Length 94;
Best Local Similarity 27.3%; Pred. No. 11;
Matches 6; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 12 KHLNSXERVEWLKKLQDVHNY 33
Db 59 KAINKLSQIEWFKKSVRDIRAF 80

RESULT 25
S26945
DNA-directed RNA polymerase (EC 2.7.7.6) - Podospora anserina mitochondrion plasmid pAL2
C:Species: mitochondrion Podospora anserina
C:Date: 06-Jan-1995 #sequence_revision 23-Feb-1996 #text_change 07-Dec-1999
C:Accession: S26945
R:Hermanns, J.; Osiewicz, H.D.
Curr. Genet. 22, 491-500, 1992
A:Title: The linear mitochondrial plasmid pAL2-1 of a long-lived Podospora anserina mutant
A:Reference number: S26945; MUID:93113721; PMID:1473181
A:Accession: S26945
A:Molecule type: DNA
A:Residues: 1-948 <HER>
A:Cross-references: UNIPARC:UPI0000175725; EMBL:X60707
A:Note: the authors translated the codons ATA as Met, CTC as Thr and CTT as Thr
A:Note: the sequence shown follows the authors' translation
C:Genetics:
A:Genome: mitochondrion plasmid pAL2-1
A:Genetic code: SGC3
C:Superfamily: phage T7 DNA-directed RNA polymerase
C:Keywords: mitochondrion; nucleotidyltransferase; transcription

Query Match 29.7%; Score 49; DB 2; Length 948;
Best Local Similarity 35.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 14 LNSXERVEWLKKLQDVHNY 33
Db 535 LSANDRIKVDKLNLMKNY 554

RESULT 26
A54103
centrosome autoantigen PCM-1 - human
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C:Accession: A54103
R:Balczon, R.; Bao, L.; Zimmer, W.E.
J. Cell Biol. 124, 783-793, 1994
A:Title: PCM-1, a 228-kD centrosome autoantigen with a distinct cell cycle distribution.
A:Reference number: A54103; MUID:94165144; PMID:8120099
A:Accession: A54103
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2024 <BAL>
A:Cross-references: UNIPROT:Q15154; UNIPARC:UPI0000072F55; GB:L27841; NID:G450276; PIDN:

Query Match 29.7%; Score 49; DB 2; Length 2024;
Best Local Similarity 38.5%; Pred. No. 2.4e+02;
Matches 15; Conservative 7; Mismatches 9; Indels 8; Gaps 3;

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85661
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-295 <STO>
A:Cross-references: UNIPROT:Q8X4W7; UNIPARC:UPI0000165734; GB:AE005174; NID:gl2514527; E85661
A:Experimental source: strain O157:H7, substrain EDL933
A:Accession: C85610
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-295 <ST2>
A:Cross-references: UNIPARC:UPI0000165734; GB:AE005174; NID:gl2514009; PIDN:AGS55343.1;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z1638; Z1198
C:Superfamily: transposase IS3

Query Match 29.1%; Score 48; DB 2; Length 295;
Best Local Similarity 29.6%; Pred. No. 48;
Matches 8; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 6 QXHNKXGKHLNSXRVWLRKQLQDVN 32
Db 33 QRHPDKRSARQDDWLKREIQRVYD 59

RESULT 39
T05866
hypothetical protein T29A15.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05866
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ho
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15455
A:Accession: T05866
A:Molecule type: DNA
A:Residues: 1-299 <BEV>
A:Cross-references: UNIPROT:Q9T085; UNIPARC:UPI00000A51C1; EMBL:AL035602
A:Experimental source: cultivar Columbia; BAC clone T29A15
C:Genetics:
A:Map position: 4
A:Introns: 62/1
A>Note: T29A15.100

Query Match 29.1%; Score 48; DB 2; Length 299;
Best Local Similarity 39.3%; Pred. No. 49;
Matches 11; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 3 SEIQXNKGKHLNSXRVWLRKQLQDV 30
Db 232 SESNYEQKSLRDGERVEMLRKEVSEL 259

RESULT 40
E69733
PSX prophage ORF xkdV - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69733
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berta
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.C.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Huilo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Toesato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69733
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-687 <KUN>
A:Cross-references: UNIPROT:P54341; UNIPARC:UPI000006028B; GB:Z99110; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: xkdV

Query Match 29.1%; Score 48; DB 2; Length 687;
Best Local Similarity 39.3%; Pred. No. 1.1e+02;
Matches 11; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY 1 SVSEIQXN--XGKHLNSXRVWLRKK 26
Db 64 SKTEFNEHNDHSDTRHITSVERDEWNAKE 91

Search completed: January 28, 2006, 01:16:43
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2006, 01:06:47 ; Search time 162 Seconds
(without alignments)
143.719 Million cell updates/sec

Title: US-09-674-597A-16
Perfect score: 165
Sequence: 1 SVSEIQXHXGKHLNEXRVEWLKQLQDVHNY 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	144.5	87.6	86	Q9N1V0	equus caball
2	144.5	87.6	115	1 PTHY HUMAN	
3	144.5	87.6	115	1 PTHY MACFA	
4	144.5	87.6	115	2 Q4VB48 HUMAN	
5	139.5	84.5	115	1 PTHY CANFA	
6	139.5	84.5	115	1 PTHY_PIG	
7	136.5	82.7	115	1 PTHY_BOVIN	
8	136.5	82.7	115	1 PTHY_FELCA	
9	127.5	77.3	105	2 Q80WZ2 RAT	
10	127.5	77.3	115	1 PTHY RAT	
11	121.5	73.6	115	2 Q9ZOL6 MOUSE	
12	96.5	58.5	119	1 PTHY CHICK	
13	71.5	43.3	91	2 Q6W9J4 FUGRU	
14	65.5	39.7	102	2 Q5TLZ1 BRARE	
15	65.5	39.7	102	2 Q6WQ25 BRARE	
16	62.5	37.9	99	2 Q6WQ24 BRARE	
17	62	37.6	1449	2 Q4RPY8 TETNG	
18	60.5	36.7	163	2 Q918E9 FUGRU	
19	60.5	36.7	391	2 Q51GF8 ENTHI	
20	59	35.8	15	1 CB30 HYDMC	
21	59	35.8	140	2 Q8BYA2 MOUSE	
22	59	35.8	926	2 Q60KX2 CAEBR	
23	59	35.8	1257	1 ARI4A HUMAN	
24	59	35.8	3678	1 DMD MOUSE	
25	58.5	35.5	166	2 Q6H9R6 PLAFE	
26	58.5	35.5	166	2 Q531Q0 PLAFE	
27	57.5	34.8	162	2 Q918U2 SPAAU	
28	57	34.5	143	2 Q5H3Y0_XANOR	
29	56.5	34.2	107	2 Q4TG14 TETNG	
30	56	33.9	193	2 Q8W2V7 ORYSA	
31	55	33.3	764	1 CFAB_GORGO	

32	55	33.3	764	1	CFAB_HUMAN	P00751	homo sapien
33	55	33.3	764	1	CFAB_PANTR	Q864w0	pan troglod
34	55	33.3	764	1	CFAB_PONPY	Q864w1	pongo pygma
35	55	33.3	764	2	Q5JF89_HUMAN	Q53f89	homo sapien
36	55	33.3	764	2	Q5JP67_HUMAN	Q53p67	homo sapien
37	55	33.3	764	2	Q5ST50_HUMAN	Q5st50	homo sapien
38	54	32.7	118	2	Q83JQ3_SHIFL	Q83jq3	shigella fl
39	54	32.7	323	2	Q7R8J7_PLAYO	Q7r8j7	plasmidium
40	54	32.7	1252	2	Q5Z1S6_CHICK	Q5z1s6	gallus gall
41	53.5	32.4	31	2	Q91Y90_PERMA	Q91y90	peromyscus
42	53.5	32.4	31	2	Q91Y91_PERPL	Q91y91	peromyscus
43	53.5	32.4	177	2	Q4RSF3_TETNG	Q4rsf3	tetradon n
44	53.5	32.4	4007	2	Q4SZ57_TETNG	Q4sz57	tetradon n
45	53	32.1	394	2	Q4UHV5_THEAN	Q4uhv5	theileria a
46	53	32.1	831	2	Q7TUQ4_PROMM	Q7tuq4	prochloroco
47	53	32.1	1245	2	Q962K7_PLAVI	Q962k7	plasmodium
48	53	32.1	3119	2	Q8IHM0_PLAF7	Q8ihm0	plasmodium
49	52.5	31.8	198	2	Q5SPK3_BRARE	Q5spk3	brachydanio
50	52.5	31.8	198	2	Q4VVA3_BRARE	Q4vva3	brachydanio
51	52.5	31.8	1011	2	Q75MD7_HUMAN	Q75md7	homo sapien
52	52.5	31.8	1235	2	Q5D049_HUMAN	Q5d049	homo sapien
53	52.5	31.8	1259	1	AUTS2_HUMAN	Q8wx7	homo sapien
54	52	31.5	182	2	Q8I996_PLAPA	Q8i996	plasmodium
55	52	31.5	367	2	Q8TJM4_METAC	Q8tjm4	methanosaarc
56	52	31.5	394	2	Q4N7Q5_THEPA	Q4n7q5	theileria p
57	52	31.5	449	2	Q8N2Q8_HUMAN	Q8n2q8	homo sapien
58	52	31.5	730	2	Q7SDF6_NEUCR	Q7sdf6	neurospora
59	52	31.5	734	2	Q4IQZ0_GIBZE	Q4iqz0	gibberella
60	52	31.5	3680	1	DMD_CANFA	Q97592	canis famli
61	52	31.5	3685	1	DMD_HUMAN	P11332	homo sapien
62	52	31.5	3685	2	Q7KZ48_HUMAN	Q7kz48	homo sapien
63	52	31.5	3685	2	Q5JYU0_HUMAN	Q5jyu0	homo sapien
64	51.5	31.2	130	2	Q70327_MESAU	Q70327	mesocricetu
65	51.5	31.2	160	2	Q923T1_SIGHI	Q923t1	sigmodon hi
66	51.5	31.2	324	2	Q4TQC7_9SPHN	Q4tqc7	erythrobact
67	51.5	31.2	908	2	Q7XEL3_ORYSA	Q7xel3	oryza sativ
68	51	30.9	105	2	Q9AFQ0_SHIFL	Q9afq0	shigella fl
69	51	30.9	117	2	Q9RP29_SHIFL	Q9rp29	shigella fl
70	51	30.9	117	2	Q9Q021_SHIFL	Q9q021	shigella fl
71	51	30.9	118	2	Q9AFX1_SHIFL	Q9afx1	shigella fl
72	51	30.9	118	2	Q9XC10_SHIFL	Q9xc10	shigella fl
73	51	30.9	118	2	Q6GZJ9_ECOLI	Q6gzj9	escherichia
74	51	30.9	118	2	Q87509_ECOLI	Q87509	escherichia
75	51	30.9	118	2	Q8FDY4_ECOL6	Q8fdy4	escherichia
76	51	30.9	118	2	Q83KQ0_SHIFL	Q83kq0	shigella fl
77	51	30.9	200	2	Q51JQ3_MAGGR	Q51jq3	magnaporthe
78	51	30.9	208	2	Q5IKI5_MAGGR	Q5iki5	magnaporthe
79	51	30.9	216	2	Q5L815_BACFN	Q5l815	bacteroides
80	51	30.9	216	2	Q64N96_BACFR	Q64n96	bacteroides
81	51	30.9	222	2	Q52E75_MAGGR	Q52e75	magnaporthe
82	51	30.9	225	2	Q8CXV7_ECOL6	Q8cxv7	escherichia
83	51	30.9	229	2	Q5LS59_MAGGR	Q5ls59	magnaporthe
84	51	30.9	240	1	T341_ECOLI	P11257	escherichia
85	51	30.9	295	2	Q7UD38_SHIFL	Q7ud38	shigella fl
86	51	30.9	295	2	Q4FBE2_ECOLI	Q4fbe2	escherichia
87	51	30.9	295	2	Q6H9S3_9CAUD	Q6h9s3	phage phi 4
88	51	30.9	296	1	T629_SHISO	P16942	shigella so
89	51	30.9	296	2	Q5IOA0_SHIBO	Q5ioa0	shigella bo
90	51	30.9	296	2	Q6SSJ4_SHIDY	Q6esj4	shigella dy
91	51	30.9	296	2	Q8VR52_ECOLI	Q8vr52	escherichia
92	51	30.9	296	2	Q8CXV4_ECOL6	Q8cxv4	escherichia
93	51	30.9	296	2	Q8CM76_ECOL6	Q8cm76	escherichia
94	51	30.9	323	2	Q7VE14_PROMA	Q7ve14	prochloroco
95	51	30.9	374	2	Q8P245_METMA	Q8p245	methanosaarc
96	51	30.9	512	2	Q7P243_CHRVO	Q7p249	chromobacte
97	51	30.9	526	2	Q649R7_9ARCH	Q649r7	uncultured
98	51	30.9	602	2	Q66UC5_9DIPT	Q66uc5	culicoides
99	51	30.9	722	2	Q52GP2_MAGGR	Q52gp2	magnaporthe
100	51	30.9	901	2	Q5B9P1_EMENI	Q5b9p1	aspergillus

ALIGNMENTS

RA Barden J.A., Cuthbertson R.M.;
RT "Stabilized NMR structure of human parathyroid hormone (1-34).";
RL Eur. J. Biochem. 215:315-321(1993).
RN [13]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE=95318084; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;
RA Marx U.C., Adermann K., Bayer P., Adermann K., Eychart A.,
RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
RA Roesch P.;
RT "Structure of human parathyroid hormone 1-37 in solution.";
RL J. Biol. Chem. 270:15194-15202(1995).
RN [14]
RP STRUCTURE BY NMR OF 32-70.
RX MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;
RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Roesch P.;
RT "Solution structures of human parathyroid hormone fragments hPTH(1-34)
and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";
RL Biochem. Biophys. Res. Commun. 267:213-220(2000).
RN [15]
RP VARIANT FIH ARG-18.
RX MEDLINE=91009811; PubMed=2212001;
RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
RA Kronenberg H.M.;
RT "Mutation of the signal peptide-encoding region of the
preparathyroid hormone gene in familial isolated
hypoparathyroidism.";
RL J. Clin. Invest. 86:1084-1087(1990).
RN [16]
RP VARIANT FIH PRO-23.
RX PubMed=10523031;
RA Sunthornheparakul T., Churesigaew S., Ngongarmratana S.;
RT "A novel mutation of the signal peptide of the preproparathyroid
hormone gene associated with autosomal recessive familial isolated
hypoparathyroidism.";
RL J. Clin. Endocrinol. Metab. 84:3792-3796(1999).
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
bone and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: Defects in PTH are a cause of familial isolated
hypoparathyroidism (FIH) [MIM:146200]. FIH exist both as autosomal
dominant and recessive forms of hypoparathyroidism.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; J00301; AAA60215.1; -; Genomic_DNA.
DR EMBL; V00597; CAA23843.1; -; mRNA.
DR EMBL; A29146; CAA01956.1; -; Unassigned_DNA.
DR FIR; A19339; PTHU.
DR PDB; 1BWV; NMR; @=32-70.
DR PDB; 1ET1; X-ray; A/B=32-65.
DR PDB; 1ET2; Model; A=32-65.
DR PDB; 1FVY; NMR; A=32-62.
DR PDB; 1HPY; NMR; @=32-68.
DR PDB; 1HPY; NMR; @=32-62.
DR PDB; 1HPY; NMR; @=32-65.
DR PDB; 1HWH; NMR; @=32-65.
DR PDB; 1ZWA; NMR; @=32-65.
DR PDB; 1ZWB; NMR; @=33-68.
DR PDB; 1ZWD; NMR; @=34-68.
DR PDB; 1ZWE; NMR; @=35-68.
DR PDB; 1ZWF; NMR; @=35-68.
DR PDB; 1ZWG; NMR; @=35-68.
DR Ensembl; ENSG00000152266; Homo sapiens.
DR HGNC; HGNC:9606; PTH.
DR MIM; 168450; -;
DR MIM; 146200; -;
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0005179; F:hormone activity; TAS.
DR GO; GO:0045453; P:bone resorption; NAS.

DR GO; GO:0006874; P:calcium ion homeostasis; NAS.
DR GO; GO:0046058; P:cAMP metabolism; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO; GO:0008628; P:induction of apoptosis by hormones; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrdorm_sub.
DR PANTHER; PTHR10541; Pthyrdorm_sub; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR PIRSF; PIRSF01832; PTH; 1.
DR ProDom; PD010687; Pthyrdorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW 3D-structure; Direct protein sequencing; Disease mutation; Hormone;
KW Signal.
FT SIGNAL. 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT VARIANT 18 18
FT VARIANT 23 23
FT CONFLICT 107 107
FT HELIX 34 64
FT SEQUENCE 115 AA; 12861 MW; 849015736A6E5597 CRC64;
Query Match 87.6%; Score 144.5; DB 1; Length 115;
Best Local Similarity 85.3%; Pred. No. 7.2e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 1 SVSEIQ-VHNTGKHLNSRVERWLRKKLQDVHNY 33
DB 32 SVSEIQVHNTGKHLNSRVERWLRKKLQDVHNF 65
RESULT 3
PTHY_MACFA
ID PTHY_MACFA STANDARD; PRT; 115 AA.
AC Q9XT35;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Malaivijitnond S., Takenaka O.;
RT "Nucleotide sequences of parathyroid gene in five species of macaque
of Thailand".
RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
bone and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF130257; AAD42777.1; -; Genomic_DNA.
DR HSSP; P01270; IET1.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrdorm_sub.

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DR PANTHER; PTHR10541; Pthyrdorm_sub; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR PIRSF; PIRSF001832; PTH; 1.
DR ProDom; PD010687; Pthyrdorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25 By similarity.
FT PROPEP 26 31 By similarity.
FT CHAIN 32 115 Parathyroid hormone.
SQ SEQUENCE 115 AA; 12890 MW; 8C2500EF24BE5597 CRC64;

Query Match 87.6%; Score 144.5; DB 1; Length 115;
Best Local Similarity 85.3%; Pred. No. 7.2e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

1 SVSEIQ-XHNKGKHLNSXERVELRKKLQDVHNY 33
2 SVSEIQLMHNLGKHLNSMERVELRKKLQDVHNF 65

RESULT 4
Q4VB48 HUMAN PRELIMINARY; PRT; 115 AA.
AC Q4VB48
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Parathyroid hormone, preproprotein.
GN Name=PTH;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udell T.B., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Umed T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC096143; AAH96143.1; -; mRNA.
DR EMBL; BC096144; AAH96144.1; -; mRNA.
DR EMBL; BC096145; AAH96145.1; -; mRNA.
DR EMBL; BC096142; AAH96142.1; -; mRNA.
DR InterPro; IPR001415; Parathyrd hrm.
DR PIRSF; PIRSF003625; Pthyrdorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrdorm_sub; 1.

Query Match 87.6%; Score 144.5; DB 1; Length 115;
Best Local Similarity 85.3%; Pred. No. 7.2e-12;
Matches 29; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

1 SVSEIQ-XHNKGKHLNSXERVELRKKLQDVHNY 33
2 SVSEIQLMHNLGKHLNSMERVELRKKLQDVHNF 65

RESULT 5
PTHY CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Parathyroid;
RX MEDLINE=953696; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C;
RA Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., Dewille J.W.,
RA Capen C.C.;
RT "Sequences of the cDNAs encoding canine parathyroid hormone-related
protein and parathyroid hormone."
RL Gene 160:241-243 (1995).
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
bone and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
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use as long as its content is in no way modified and this statement is not
removed.
CC EMBL; U15662; AAA82584.1; -; mRNA.
DR PIR; JC4202; JC4202.
DR HSSP; P01268; 1ZWC.
DR Ensembl; ENSCAPG00000008177; Canis familiaris.
DR InterPro; IPR001415; Parathyrd hrm.
DR InterPro; IPR003625; Pthyrdorm_sub.
DR PANTHER; PTHR10541; Pthyrdorm_sub; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR PIRSF; PIRSF001832; PTH; 1.
DR ProDom; PD010687; Pthyrdorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25 By similarity.
FT PROPEP 26 31 By similarity.
FT CHAIN 32 115 Parathyroid hormone.
SQ SEQUENCE 115 AA; 12957 MW; FC38F77F1C8CFE56 CRC64;

Query Match 84.5%; Score 139.5; DB 1; Length 115;
Best Local Similarity 82.4%; Pred. No. 3.5e-11;
Matches 28; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

1 SVSEIQ-XHNKGKHLNSXERVELRKKLQDVHNY 33
2 SVSEIQFMHNLGKHLNSMERVELRKKLQDVHNF 65

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RESULT 6
PTHY_PIG
ID PTHY_PIG STANDARD; PRT; 115 AA.
AC P01269;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87116938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
RL preproparathyroid hormone from pig and rat.";
RL Nucleic Acids Res. 15:6740-6740(1987).
RN [2]
RP PROTEIN SEQUENCE OF 26-115.
RX MEDLINE=76018954; PubMed=1164500;
RA Chu L.L.H., Huang W.-Y., Littlelike E.T., Hamilton J.W., Cohn D.V.;
RT "Porcine parathyroid hormone. Identification, biosynthesis, and
RL partial amino acid sequence.";
RL Biochemistry 14:3631-3635(1975).
RN [3]
RP PROTEIN SEQUENCE OF 32-115.
RX MEDLINE=74253317; PubMed=4840833;
RA Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA Potts J.T. Jr.;
RT "The amino acid sequence of porcine parathyroid hormone.";
RL Biochemistry 13:1994-1999(1974).
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC bone and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
CC
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CC removed.
CC
CC EMBL; X05722; CAA29193.1; -; mRNA.
CC
CC PIR; B26806; PTPG.
CC
CC DR HSSP; P01270; 1BMX.
CC
CC DR InterPro; IPR001415; Parathyroid hrm.
CC
CC DR InterPro; IPR003625; Pthyhorm_sub.
CC
CC DR PANTHER; PTHR10541; Pthyhorm_sub; 1.
CC
CC DR Pfam; PF01279; Parathyroid; 1.
CC
CC DR PIRSF; PIRSF001832; PTH; 1.
CC
CC DR ProDom; PD010687; Pthyhorm_sub; 1.
CC
CC DR SMART; SM00087; PTH; 1.
CC
CC DR PROSITE; PS00335; PARATHYROID; 1.
CC
CC KW Direct protein sequencing; Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 Parathyroid hormone.
FT SQ SEQUENCE 115 AA; 12852 MW; 9FEBBCDE614BAC16 CRC64;

Query Match 84.5%; Score 139.5; DB 1; Length 115;
Best Local Similarity 82.4%; Pred. No. 3.5e-11;
Matches 28; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHXGKHLNSXERVWLKKLODVNY 33
Db 32 SVSEIQMLNKLHSLSSRVEWLKKLODVHNF 65

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RESULT 7
PTHY_BOVIN
ID PTHY_BOVIN STANDARD; PRT; 115 AA.
AC P01268;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=80056617; PubMed=388425;
RA Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
RA Potts J.T. Jr., Rich A.;
RT "Cloning and nucleotide sequence of DNA coding for bovine
RL preproparathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82037785; PubMed=6170060;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Introduction by molecular cloning of artifactual inverted sequences
RL at the 5' terminus of the sense strand of bovine parathyroid hormone
RL cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83105964; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL Mol. Cell. Endocrinol. 28:411-424(1982).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84262483; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5;
RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT "Isolation and complete nucleotide sequence of the gene for bovine
RL parathyroid hormone.";
RL Gene 28:319-329(1984).
RN [5]
RP PROTEIN SEQUENCE OF 26-115.
RX MEDLINE=74142666; PubMed=4522780;
RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
RA Cohn D.V.;
RT "The N-terminal amino-acid sequence of bovine parathyroid
RL hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN [6]
RP PROTEIN SEQUENCE OF 32-115.
RX MEDLINE=71076162; PubMed=5531031;
RA Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
RA Aurbach G.D., Potts J.T. Jr.;
RT "The amino acid sequence of bovine parathyroid hormone I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN [7]
RP PROTEIN SEQUENCE OF 32-115.
RX MEDLINE=71063634; PubMed=5275384;
RA Brewer H.B. Jr., Ronan R.;
RT "Bovine parathyroid hormone: amino acid sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE=71091588; PubMed=4322265;
RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RA Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RT "Synthesis of a biologically active N-terminal tetraoctapeptide
RL of parathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN [9]

```


RC TISSUE=Thyroid;
 RG NIH MGC Project;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF066075; AAC99656.1; -; Genomic DNA.
 DR EMBL; BC099456; AAH99456.1; -; mRNA.
 DR HSSP; P01270; LZWB.
 DR Ensemble; ENSMUSG00000059077; Mus musculus.
 DR MGI; MGI:97799; Pth.
 DR GO; GO:0005615; C:extracellular space; IDA.
 DR GO; GO:0005179; F:hormone activity; IDA.
 DR GO; GO:0006874; P:calcium ion homeostasis; TAS.
 DR InterPro; IPR001415; Parathyroid hrm.
 DR PANTHER; PTHR10541; Pthyrhorm_sub.
 DR Pfam; PF01279; Parathyroid; 1.
 DR PIRSF; PIRSF001832; PTH; 1.
 DR ProDom; PD010687; Pthyrhorm_sub; 1.
 DR SMART; SM00087; PTH; 1.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW SIGNAL.
 FT SIGNAL
 FT CHAIN 1 25 Potential.
 FT CHAIN 32 115 parathyroid hormone.
 SQ SEQUENCE 115 AA; 12825 MW; DA43FABBCB4E2FD9 CRC64;
 Query Match 73.6%; Score 121.5; DB 2; Length 115;
 Best Local Similarity 67.6%; Pred. No. 1.1e-08;
 Matches 23; Conservative 6; Mismatches 4; Indels 1; Gaps 1;
 QY 1 SVSBIQ-XHNKXGKHLNSXERVEWLRKQLQDVHNY 33
 :|||||:|||||:|||||:|||||:|||||:
 Db 32 AVSHIQLMHLNGLKHLASMERQWLRLKQLQDMHNF 65
 RESULT 12
 PTHY CHICK
 ID PTHY CHICK STANDARD; PRT; 119 AA.
 AC P15743;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Parathyroid Hormone precursor (PTH).
 GN Name=PTH;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphia; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodonidae; Tetraodontidae; Takifugu.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89219100; PubMed=2710135;
 RA Russell J., Sherwood L.M.;
 RT "Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid hormone mRNA and the deduced sequence of the hormone precursor.";
 RL Mol. Endocrinol. 3:325-331(1989).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89284968; PubMed=3251402;
 RA Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
 RA Kronenberg H.M.;
 RT "Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.";
 RL J. Bone Miner. Res. 3:689-698(1988).
 CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; M31604; AAA49093.1; -; mRNA.
 DR EMBL; M36522; AAB02866.1; -; mRNA.
 DR FIR; A34937; A34937.
 DR HSSP; P01270; IFVY.
 DR Ensemble; ENSGALG00000005358; Gallus gallus.
 DR InterPro; IPR001415; Parathyroid hrm.
 DR InterPro; IPR003626; PTH related.
 DR InterPro; IPR003625; Pthyrhorm_sub.
 DR PANTHER; PTHR10541; Pthyrhorm_sub; 1.
 DR Pfam; PF01279; Parathyroid; 1.
 DR PIRSF; PIRSF001832; PTH; 1.
 DR ProDom; PD013225; PTH related; 1.
 DR ProDom; PD010687; Pthyrhorm_sub; 1.
 DR SMART; SM00087; PTH; 1.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW Hormone; Signal.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 119 Parathyroid hormone.
 SQ SEQUENCE 119 AA; 13943 MW; B309D8E772997F6E CRC64;
 Query Match 58.5%; Score 96.5; DB 1; Length 119;
 Best Local Similarity 57.6%; Pred. No. 3e-05;
 Matches 19; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
 QY 1 SVSBIQ-XHNKXGKHLNSXERVEWLRKQLQDVHN 32
 :|||||:|||||:|||||:|||||:|||||:
 Db 32 SVSEIQLMHLNGLKHLASMERQWLRLKQLQDVHS 64
 RESULT 13
 Q6W9J4_FUGRU
 ID Q6W9J4_FUGRU PRELIMINARY; PRT; 91 AA.
 AC Q6W9J4;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Parathyroid hormone type-2.
 GN Name=PTH;
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphia; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodonidae; Tetraodontidae; Takifugu.
 OC NCBI_TaxID=31033;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14684608; DOI=10.1210/en.2003-0964;
 RA Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
 RA Bastape M., Rubin D.A., Juppner H.;
 RT "Identification and characterization of two parathyroid hormone-like molecules in zebrafish.";
 RT molecules in zebrafish.";
 RL Endocrinology 145:1634-1639(2004).
 DR EMBL; AY302221; AAQ73561.1; -; Genomic DNA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0007595; P:lactation; IEA.
 DR InterPro; IPR001415; Parathyroid hrm.
 DR InterPro; IPR003625; Pthyrhorm_sub.
 DR InterPro; IPR003626; PTH related.
 DR PANTHER; PTHR10541; Pthyrhorm_sub; 1.
 DR Pfam; PF01279; Parathyroid; 1.
 DR ProDom; PD010687; Pthyrhorm_sub; 1.
 DR ProDom; PD013225; PTH related; 2.
 DR SMART; SM00087; PTH; 1.
 SQ SEQUENCE 91 AA; 10647 MW; 75BBA25CEA64BF68 CRC64;
 Query Match 43.3%; Score 71.5; DB 2; Length 91;
 Best Local Similarity 45.2%; Pred. No. 0.062;
 Matches 14; Conservative 8; Mismatches 8; Indels 1; Gaps 1;
 QY 1 SVSBIQ-XHNKXGKHLNSXERVEWLRKQLQDV 30

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DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrdorm_sub; 1.
DR SMART; SM00087; PTH; 1.
SQ SEQUENCE 102 AA; 11690 MW; 5AA7A84FF4110764 CRC64;

Query Match 39.7%; Score 65.5; DB 2; Length 102;
Best Local Similarity 40.6%; Pred.No. 0.46;
Matches 13; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNXGKHLNSXERVEWLKKLDVH 31
   :|:|:| | | | | | | | | | | | | |
Db 36 AVNEVQLMHNLVGHVKKHQLRQDWLQMKLRGIH 67

RESULT 16
Q6WQ24_BRARE
ID Q6WQ24 BRARE PRELIMINARY; PRT; 99 AA.
AC Q6WQ24;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Parathyroid hormone ligand type-2.
GN Name=pth2;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE..
RX PubMed=14684608; DOI=10.1210/en.2003-0964;
RA Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
RA Bastepe M., Rubin D.A., Juppner H.;
RT "Identification and characterization of two parathyroid hormone-like
RT molecules in zebrafish."
RL Endocrinology 145:1634-1639(2004).
DR EMBL; AY275670; AAQ16567.1; -; mRNA.
DR ZFIN; ZDB-GENE-040623-2; pth2.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrdorm_sub.
DR PANTHER; PTHR10541; Pthyrdorm_sub; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrdorm_sub; 1.
DR SMART; SM00087; PTH; 1.
SQ SEQUENCE 99 AA; 11569 MW; 7FBFE84A7CA462 CRC64;

Query Match 37.9%; Score 62.5; DB 2; Length 99;
Best Local Similarity 38.7%; Pred.No. 1.2;
Matches 12; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNXGKHLNSXERVEWLKKLDVH 30
   :|:|:| | | | | | | | | | | | | |
Db 34 SISEVQLMHNVRSHKEMLDQDWLQKLNNI 64

RESULT 17
Q4RPY8_TETNG
ID Q4RPY8 TETNG PRELIMINARY; PRT; 1449 AA.
AC Q4RPY8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 17 SCAF15006, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0030867001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;

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RN NP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud C., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Bernardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Croliius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01015006; CAG09544.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 1449 AA; 157867 MW; E1608E07DA30F7DC CRC64;

Query Match 37.6%; Score 62; DB 2; Length 1449;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 14 LNSXRVWLKRLKLDVHNY 33
Db 1373 MNSLERSFLOKLDIRNH 1392

RESULT 18
Q918E9 FUGRU
ID Q918E9 FUGRU PRELIMINARY; PRT; 163 AA.
AC Q918E9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE Parathyroid hormone-related protein precursor.
GN Names:PTHrP;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphia; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20314478; PubMed=10854780; DOI=10.1016/S0378-1119(00)00167-0;
RX Power D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,
RX Elgar G., Clark M.S.;
RT "Genomic structure and expression of parathyroid hormone-related
RT protein in a teleost, Fugu rubripes."
RL Gene 250:67-76(2000).
RL EMBL; Auz49391; CAB94712.1; -; Genomic_DNA.
DR HSP; F12272; 1BZG.
DR Ensembl; SINFUG000000131728; Fugu rubripes.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007595; P:lactation; IEA.
DR InterPro; IPR001415; Parathyrd hrm.
DR InterPro; IPR003626; PTH related.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD013225; PTH_related; 1.
KW Signal.
FT SIGNAL 1 34 Potential.
SQ SEQUENCE 163 AA; 18698 MW; 3ACSF2C764732278 CRC64;

```

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Query Match 36.7%; Score 60.5; DB 2; Length 163;
Best Local Similarity 43.8%; Pred. No. 3.6;
Matches 14; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

Qy 1 SVSEIQ-KHNKGKHLNSXRVWLKRLKLDVH 31
Db 38 SVSHAQLMHDKGRSLQEFRRRWLHLKLEEVH 69

RESULT 19
Q51GF8 ENTHI
ID Q51GF8 ENTHI PRELIMINARY; PRT; 391 AA.
AC Q51GF8;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DE Eukaryotic initiation factor 4A, putative.
GN ORFNames=3.t00028;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoef U., Bhattacharya A.,
RA Chillingworth T., Church C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Slicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the DEAD box helicase family.
DR EMBL; AAFB01000013; EAL51901.1; -; Genomic_DNA.
DR GO; GO:0003743; F:translation initiation factor activity; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR000629; DEAD box_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR PROSITE; PS00039; DEAD ATP HELICASE; 1.
KW ATP-binding; Helicase; Hydrolase; Initiation factor;
KW Nucleotide-binding; RNA-binding.
SQ SEQUENCE 391 AA; 44041 MW; 22107ADBFE46EF93 CRC64;

Query Match 36.7%; Score 60.5; DB 2; Length 391;
Best Local Similarity 57.9%; Pred. No. 8.9;
Matches 11; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

Qy 15 NSXRVWLKRLKLDVHNY 33
Db 265 NSKNRVWLKRLKLDVHNY 282

RESULT 20
CB30 HYDMC
ID CB30 HYDMC STANDARD; PRT; 15 AA.
AC P83630;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)

```

DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Chitin-binding protein HM30 (Fragment).
 OS Hydrangea macrophylla (Bigleaf hydrangea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; Cornales; Hydrangeaceae; Hydrangea.
 OX NCBI_TaxID=23110;
 RN
 RP PROTEIN SEQUENCE, FUNCTION, INDUCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Leaf;
 RX MEDLINE=21671918; PubMed=11812226; DOI=10.1006/prep.2001.1551;
 RA Yang Q., Gong Z.-Z.;
 RT "Purification and characterization of an ethylene-induced antifungal
 RT protein from leaves of Guilder rose (Hydrangea macrophylla).";
 RL Protein Expr. Purif. 24:76-82(2002).
 CC -!- FUNCTION: Has antifungal activity against A.alternate,
 CC A.cucumerina, A.niger, C.gossypii, F.oxysporum, F.oxysporum subsp
 CC melonis, F.moniliforme, F.cucumeris, and V.dahliae. Has no
 CC chitinase or agglutination activities.
 CC -!- INDUCTION: By ethylene.
 CC -!- MASS SPECTROMETRY: MW=30010; METHOD=Electrospray; RANGE=1-?;
 CC NOTE=Ref.1.
 CC
 CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
 CC -!- CAUTION: 14 of the 15 residues are identical to an internal region
 CC of human parathyroid hormone. That seems quite an incredible
 CC "coincidence".
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC Antimicrobial: Chitin-binding; Direct protein sequencing; Fungicide.
 KW NON_TER 15 15
 FT SEQUENCE 15 AA; 1875 MW; 7BE51BEC7D5B84DD CRC64;
 SQ

Query Match 35.8%; Score 59; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.51;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 NSXERVEWRKKLQD 29
 || |||||
 Db 1 NSMERVEELRKKLQD 15

RESULT 21
 Q8BYA2 MOUSE
 ID Q8BYA2 MOUSE PRELIMINARY; PRT; 140 AA.
 AC Q8BYA2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
 DE library, clone:A63009N03 product:RETINOBLASTOMA-BINDING PROTEIN 1
 DE (RBBP-1) homolog (Fragment).
 GN Name:Arid4a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Niehi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuoka H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
 RA Fukuda S., Furuno M., Hanagaki T., Hiraoka T., Hirozane T.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kasukawa T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akai H., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK041444; BAC30948.1; -; mRNA.
 DR Ensembl; ENSMUSG0000034629; Mus musculus.
 DR MGI; MGI:2444354; Arid4a.
 RP NON_TER 1 1
 SQ SEQUENCE 140 AA; 15988 MW; 15CE80236A5E9930 CRC64;

Query Match 35.8%; Score 59; DB 2; Length 140;

Best Local Similarity 42.9%; Pred. No. 5;
Matches 9; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 13 HLNSEVEREWLKKLODVHNY 33
Db 62 NNNSTERISFLQELQIRKY 82

RESULT 22

Q60KX2 CAEBR
ID Q60KX2 CAEBR PRELIMINARY; PRT; 926 AA.
AC Q60KX2;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein CBG23865.
GN Name=CBG23865;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
ON NCBI_TaxID=6238;
RX NCBI
[1]
RP NUCLEOTIDE SEQUENCE
RG The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAC01000197; CAE56230.1; -; Genomic DNA.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; ZnfRING.
DR PROSITE; PS50089; ZfRING 2; 1.
KW Hypothetical protein; Metal-binding; Nuclear protein; Zinc;
KW Zinc-finger.
SQ SEQUENCE 926 AA; 106547 MW; 989B11391F8AB4BA CRC64;

Query Match 35.8%; Score 59; DB 2; Length 926;
Best Local Similarity 38.7%; Pred. No. 35;
Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 SVSEIQHNKXHLNSEVEREWLKKLODVH 31
Db 372 SVSEIPIRHNGGDYFISMEDVWVKAKWKY 402

RESULT 23

ARI4A HUMAN
ID ARI4A HUMAN STANDARD; PRT; 1257 AA.
AC P29374; Q15991; Q15992; Q15993;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE AT-rich interactive domain-containing protein 4A (ARID domain-containing protein 4A) (Retinoblastoma-binding protein 1) (RBBP-1).
GN Name=ARI4A; Synonyms=RBBP1, RBPI;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
ON NCBI_TaxID=9606;
RX NCBI
[1]
RP NUCLEOTIDE SEQUENCE (ISOFORM I).
EX MEDLINE=94020841; PubMed=8414517;
RA Fattaey A.R., Helin K., Dembski M.S., Dyson N., Harlow E.,
RA Vuocolo G.A., Hanobik M.G., Haskell K.M., Oloff A., Defeo-Jones D.,
RA Jones R.E.;
RT "Characterization of the retinoblastoma binding proteins RBP1 and
RT RBP2.";
RL Oncogene 8:3149-3156(1993).

RN [2]
RP NUCLEOTIDE SEQUENCE, SUBCELLULAR LOCATION, AND ALTERNATIVE SPLICING.
RX MEDLINE=93205410; PubMed=8455946;
RA Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.;
RT "Alternative splicing of the RBP1 gene clusters in an internal exon
RT that encodes potential phosphorylation sites.";
RL Oncogene 8:949-957(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 855-1203 (ISOFORM I).
RX MEDLINE=91312450; PubMed=1857421; DOI=10.1038/352251a0;
RA Defeo-Jones D., Huang P.S., Jones R.E., Haskell K.M., Vuocolo G.A.,
RA Hanobik M.G., Huber H.E., Oloff A.;
RT "Cloning of cDNAs for cellular proteins that bind to the
RT retinoblastoma gene product.";
RL Nature 352:251-254(1991).
RN [4]
RP PHOSPHORYLATION SITE SER-1109.
RX PubMed=15302935; DOI=10.1073/pnas.0404720101;
RA Beausoleil S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,
RA Li J., Cohn M.A., Cantley L.C., Gygi S.P.;
RT "Large-scale characterization of HeLa cell nuclear phosphoproteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).
CC -! FUNCTION: Interacts with the viral protein-binding domain of the
CC retinoblastoma protein.
CC -! SUBCELLULAR LOCATION: Nuclear.
CC -! ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=I;
CC IsoId=P29374-1; Sequence=Displayed;
CC Name=II;
CC IsoId=P29374-2; Sequence=VSP_004373;
CC Name=III;
CC IsoId=P29374-3; Sequence=VSP_004371, VSP_004372;
CC -! SIMILARITY: Contains 1 ARID domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; S66427; AAB28543.1; -; mRNA.
CC EMBL; S57153; AAB25833.1; -; mRNA.
CC EMBL; S57160; AAB25834.1; -; mRNA.
CC EMBL; S57162; AAB25835.2; -; mRNA.
CC EIR; I58383; I58383.
CC HSP; Q24573; IIC20.
CC Ensembl; ENSG00000032219; Homo sapiens.
CC HGNC; HGNC:9885; ARID4A.
CC MIM; 180201; -;
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:000515; F:protein binding; TAS.
CC GO; GO:0003700; F:transcription factor activity; TAS.
CC GO; GO:0006366; P:transcription from RNA polymerase II promoter; TAS.
CC InterPro; IPR001606; ARID.
CC InterPro; IPR000953; Chromo.
CC InterPro; IPR012603; RBBINT.
CC InterPro; IPR002999; Tudor.
CC Pfam; PF01388; ARID; 1.
CC Pfam; PF08169; RBBINT; 1.
CC SMART; SM00501; BRIGHT; 1.
CC SMART; SM00298; CHROMO; 1.
CC SMART; SM00333; TUDOR; 1.
CC PROSITE; PS51011; ARID; 1.
CC Alternative splicing; Nuclear protein; Phosphorylation; Transcription;
CC Transcription regulation.
CC DOMAIN 309 401
CC REGION 951 964
CC ARID.
CC Retinoblastoma protein binding
CC (potential).
CC Phosphoserine.
CC Missing (in isoform III).
CC /FTid=VSP_004371.
CC
CC MOD_RES 1109 1109
CC VARSPLIC 1106 1174
CC
CC VARSPLIC 1121 1174
CC Missing (In isoform II).

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FT VARSPLIC 1175 1175 /FTId=VSP_004373.
FT N -> D (in isoform III).
FT /FTId=VSP_004372.
FT L -> V (in Ref. 2).
FT CONFLICT 385 385
FT CONFLICT 618 618 S -> R (in Ref. 2).
FT CONFLICT 653 653 K -> V (in Ref. 2).
FT CONFLICT 779 779 A -> T (in Ref. 2).
FT CONFLICT 1178 1178 D -> S (in Ref. 3).
FT CONFLICT 1196 1201 IRKYYM -> SENIICL (in Ref. 3).
FT CONFLICT 1257 1257 AA; F5C0AB6D6ED431DC CRC64;
SQ SEQUENCE 1257 AA; 142667 MW; 55020866D6ED431DC CRC64;

Query Match 35.8%; Score 59; DB 1; Length 1257;
Best Local Similarity 42.9%; Pred. No. 47;
Matches 9; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 13 HLNSEXVEWLRKKLQDVHNY 33
Db 1179 NNMSTERISFLQEKLEIRKY 1199

RESULT 24
DMD MOUSE
ID DMD_MOUSE STANDARD; PRT; 3678 AA.
AC P11531; Q35653; Q60703;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Dystrophin.
GN Name=Dmd;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92253376; PubMed=1579466;
RA Bies R.D., Phelps S.F., Cortez M.D., Roberts R., Caskey C.T.,
RA Chamberlain J.S.;
RT "Human and murine dystrophin mRNA transcripts are differentially
RT expressed during skeletal muscle, heart, and brain development.";
RL Nucleic Acids Res. 20:1725-1731(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 1-201.
RX MEDLINE=87273512; PubMed=3607877; DOI=10.1016/0092-8674(87)90504-6;
RA Koenig M., Hoffman E.P., Bertelson C.J., Monaco A.P., Feener C.,
RA Kunkel L.M.;
RT "Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and
RT preliminary genomic organization of the DMD gene in normal and
RT affected individuals.";
RL Cell 50:509-517(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 120-176.
RC STRAIN=129/J;
RX MEDLINE=92182520; PubMed=1543903;
RA Maconochie M.K., Brown S.D.M., Greenfield A.J.;
RT "Sequence analysis of two exons from the murine dystrophin locus.";
RL Mamm. Genome 2:64-68(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 300-1390.
RX MEDLINE=88018015; PubMed=3659917;
RA Hoffman E.P., Monaco A.P., Feener C.C., Kunkel L.M.;
RT "Conservation of the Duchenne muscular dystrophy gene in mice and
RT humans.";
RL Science 238:347-350(1987).
RN [5]
RP NUCLEOTIDE SEQUENCE OF 986-1056.
RC STRAIN=C57BL/10; TISSUE=Skeletal muscle;
RX MEDLINE=94154933; PubMed=811539;
RA Chamberlain J.S., Phelps S.F., Cox G.A., Maichele A.J.,
RA Greenwood A.D.;
RT "PCR analysis of muscular dystrophy in mdx mice.";
RL Mol. Cell Biol. Hum. Dis. Ser. 3:167-189(1993).
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RN [6]
RX NUCLEOTIDE SEQUENCE OF 3069-3181.
RP PubMed=1377655;
RA Rapaport D., Lederfein D., den Dunnen J.T., Grootsholten P.M.,
RA van Ommen G.J., Fuchs O., Nudel U., Yaffe D.;
RT "Characterization and cell type distribution of a novel, major
RT transcript of the Duchenne muscular dystrophy gene.";
RL Differentiation 49:187-193(1992).
RN [7]
RP ALTERNATIVE SPLICING.
RC STRAIN=C57BL/10; TISSUE=Retina;
RX MEDLINE=95360002; PubMed=7633443;
RA D'Souza V.N., Nguyen T.M., Morris G.E., Karges W., Pillers D.-A.M.,
RA Ray P.N.;
RT "A novel dystrophin isoform is required for normal retinal
RT electrophysiology.";
RL Hum. Mol. Genet. 4:837-842(1995).
RN [8]
RP INTERACTION WITH SNTA1.
RX MEDLINE=96032613; PubMed=7547961;
RA Madhavan R., Jarrett H.W.;
RT "Interactions between dystrophin glycoprotein complex proteins.";
RL Biochemistry 34:12204-12209(1995).
RN [9]
RP INTERACTION WITH SNTB1.
RX MEDLINE=97362062; PubMed=9214383; DOI=10.1083/jcb.138.1.81;
RA Peters M.F., Adams M.E., Froehner S.C.;
RT "Differential association of syntrophin pairs with the dystrophin
RT complex.";
RL J. Cell Biol. 138:81-93(1997).
RN [10]
RX FUNCTION: May play a role in anchoring the cytoskeleton to the
RX plasma membrane.
CC CC
RN [11]
RX SUBUNIT: Interacts with the syntrophins SNTA1, SNTB1, SNTB2, SNTC1
CC and SNTG2.
CC CC
RN [12]
RX INTERACTION:
RX Q61234:Snta1; NbExp=1; IntAct=EBI-295928, EBI-295952;
CC CC
RN [13]
RX ALTERNATIVE PRODUCTS:
RX Event=Alternative splicing; Named isoforms=1;
CC Comment=At least 11 isoforms are produced;
CC CC
RN [14]
RX Name=1;
RX IsoId=P11531-1; Sequences=Displayed;
CC CC
RN [15]
RX TISSUE SPECIFICITY: Differentially expressed during skeletal
RX muscle, heart, and brain development. Also expressed in retina.
CC CC
RN [16]
RX SIMILARITY: Contains 2 CH (calponin-homology) domains.
CC CC
RN [17]
RX SIMILARITY: Contains 22 spectrin repeats.
CC CC
RN [18]
RX SIMILARITY: Contains 1 WW domain.
CC CC
RN [19]
RX SIMILARITY: Contains 1 WW-type zinc finger.
CC CC
RN [20]
RX This Swiss-Prot entry is copyright. It is produced through a collaboration
RX between the Swiss Institute of Bioinformatics and the EMBL outstation -
RX the European Bioinformatics Institute. There are no restrictions on its
RX use as long as its content is in no way modified and this statement is not
RX removed.
CC CC
RN [21]
RX EMBL; M68859; AAB02797.1; -; mRNA.
DR EMBL; X58153; CAA41157.1; -; Genomic_DNA.
DR EMBL; M18025; AAB37530.1; -; mRNA.
DR EMBL; U56724; AAB01216.1; -; Genomic_DNA.
DR EMBL; U15218; AAA87068.1; -; mRNA.
DR PIR; S28916; S28916.
DR HSSP; P11532; 1EG3.
DR SMR; P11531; 9-246, 3040-3299.
DR IntAct; P11531; -
DR Ensembl; ENSMUSG00000045103; Mus musculus.
DR MGI; MGI:94909; Dmd.
DR GO; GO:0005626; C:insoluble fraction; IDA.
DR GO; GO:0005792; C:microsome; IDA.
DR GO; GO:0042383; C:sarcolemma; TAS.
DR GO; GO:0045202; C:synapse; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007517; P:muscle development; IMP.
DR InterPro; IPR001589; Actnin actin bd.
DR InterPro; IPR001715; Calponin_act_bd.
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DR InterPro; IPR011992; EF-Hand type.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001202; WW_Rp5_WWP.
DR InterPro; IPR000433; ZnF_Zz.
DR Pfam; PF00307; CH; 2.
DR Pfam; PF00435; Spectrin; 18.
DR Pfam; PF00397; WW; 1.
DR Pfam; PF00569; ZZ; 1.
DR SMART; SM00033; CH; 2.
DR SMART; SM00150; SPEC; 22.
DR SMART; SM00456; WW; 1.
DR SMART; SM00291; ZnF_Zz; 1.
DR PROSITE; PS00019; ACTININ_1; 1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS00021; CH; 2.
DR PROSITE; PS01159; WW_DOMAIN_1; 1.
DR PROSITE; PS01357; WW_DOMAIN_2; 1.
DR PROSITE; PS01357; ZF_Zz_1; 1.
DR PROSITE; PS01357; ZF_Zz_2; 1.
KW Actin-binding; Repeat; Calcium; Cytoskeleton;
KW Metal-binding; Repeat; Structural protein; Zinc; Zinc-finger.
FT DOMAIN 1 240
FT DOMAIN 15 119
FT DOMAIN 134 237
FT REPEAT 341 449
FT REPEAT 450 558
FT REPEAT 561 669
FT REPEAT 721 830
FT REPEAT 832 936
FT REPEAT 945 1047
FT REPEAT 1050 1156
FT REPEAT 1159 1265
FT REPEAT 1268 1369
FT REPEAT 1470 1570
FT REPEAT 1573 1678
FT REPEAT 1681 1782
FT REPEAT 1879 1981
FT REPEAT 2013 2103
FT REPEAT 2106 2210
FT REPEAT 2213 2318
FT REPEAT 2468 2570
FT REPEAT 2573 2679
FT REPEAT 2682 2795
FT REPEAT 2798 2900
FT REPEAT 2902 2924
FT REPEAT 2927 3033
FT DOMAIN 3048 3081
FT ZN_FING 3300 3347
FT REGION 3459 3511
FT CONFLICT 463 463
FT CONFLICT 677 677
FT CONFLICT 2337 2337
SQ SEQUENCE 3678 AA; 425817 MW; 1D2B74CF7DB035EE CRC64;

Query Match 35.8%; Score 59; DB 1; Length 3678;
Best Local Similarity 40.6%; Pred. No. 1.4e+02;
Matches 13; Conservative 7; Mismatches 10; Indels 2; Gaps 1;

QY 1 SVSEIQXHNKXGKHLNS--XERVEWLRKKLQDV 30
Db 1425 SLEEMKKNQGDANQRVLSQIDVAQKQLQDV 1456

RESULT 25
QH9R6_PLAFA
ID Q6H9R6_PLAFA PRELIMINARY; PRT; 166 AA.
AC Q6H9R6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Parathyroid hormone-related protein precursor.
GN Name=pthrp;
OS Platichthys flesus (European flounder).

Query Match 35.5%; Score 58.5; DB 2; Length 166;
Best Local Similarity 40.6%; Pred. No. 7;
Matches 13; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSXERVEWLRKKLQDVH 31
Db 38 SVSHAQMHDKGRSLQEFKRMWMLQELLEVEH 69

RESULT 26
Q53IQ0_PLAFA
ID Q53IQ0_PLAFA PRELIMINARY; PRT; 166 AA.
AC Q53IQ0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Parathyroid hormone-related protein precursor.
GN Name=pthrp;
OS Platichthys flesus (European flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Pleuronectidae; Platichthys.
OX NCBI_TaxID=8260;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spinal cord;
RA Lu W., McCrohan C.R., Riccardi D., Balmert R.J.;
RT "Differential expression of multi-neuropeptides in caudal
RT neurosecretory system of the euryhaline flounder (Platichthys
RT flesus).";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spinal cord;
RA Lu W., McCrohan C.R., Riccardi D., Balmert R.J.;
RT "Expression profile of Pthrp in osmoregulatory organs following
RT transfer of the euryhaline flounder (Platichthys flesus) between
RT seawater and fresh water.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spinal cord;
RA Ingleton P.M., Sidorova A., Balmert R.;
RT "Parathyroid hormone related protein in flounder.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Clark M.S.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ571691; CA500492.1; -; mRNA.
DR EMBL; AJ571691; CAD58826.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; P:hormone activity; IEA.
DR GO; GO:0007595; P:lactation; IEA.
DR InterPro; IPR001415; Parathyroid_hrm.
DR InterPro; IPR003626; PTH_related.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD013225; PTH_related; 1.
DR SMART; SM00087; PTH; 1.
KW SIGNAL.
FT CHAIN 1 25 Potential.
FT CHAIN 38 166 parathyroid hormone-related protein.
SQ SEQUENCE 166 AA; 19220 MW; 595B5520708BE300 CRC64;

Query Match 35.5%; Score 58.5; DB 2; Length 166;
Best Local Similarity 40.6%; Pred. No. 7;
Matches 13; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKXGKHLNSXERVEWLRKKLQDVH 31
Db 38 SVSHAQMHDKGRSLQEFKRMWMLQELLEVEH 69

RESULT 26
Q53IQ0_PLAFA
ID Q53IQ0_PLAFA PRELIMINARY; PRT; 166 AA.
AC Q53IQ0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Parathyroid hormone-related protein precursor.
GN Name=pthrp;
OS Platichthys flesus (European flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Pleuronectidae; Platichthys.
OX NCBI_TaxID=8260;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RA Lu W., Smyrnias I., McCrohan C.R., Balmert R.J., Riccardi D.;

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FT NON_TER 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11698 MW; 10P61F8629D06FB3 CRC64;

Query Match
Best Local Similarity 34.2%; Score 56.5; DB 2; Length 107;
Matches 13; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXRVWLKRLQDVH 31
Db 3 SVAHTQLMHDKGRITLQDFKRRMWLQELLDVH 34

RESULT 30
Q8W2V7 Oryza
ID Q8W2V7 Oryza PRELIMINARY; PRT; 193 AA.
AC Q8W2V7_Q7XFE7;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Hypothetical protein OSJNB0076H04.16.
GN ORFNames=OSJNB0076H04.16;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsitrin T., Riggs F., Hsiao J., Ziemann V., Blunt S., Pai G.,
RA VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN 2
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
[3]
RN 3
RP NUCLEOTIDE SEQUENCE.
RA The Rice Chromosome 10 Sequencing Consortium;
RA "In-depth view of structure, activity, and evolution of rice
RA chromosome 10.";
RA Science 300:1566-1569 (2003).
[4]
RN 4
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC093093; AAL58135.1; -; Genomic DNA.
DR EMBL; AB017082; AAP53279.1; -; Genomic DNA.
DR Gramene; Q8W2V7; -.
KW Hypothetical protein.
SQ SEQUENCE 193 AA; 21127 MW; 9B6053ACE1A7041C CRC64;

Query Match
Best Local Similarity 33.9%; Score 56; DB 2; Length 193;
Matches 9; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 3 SEIQXNKGKHLNSXRVWLKRLQDVH 31
Db 104 SAIEFHTLYYHKTKRVWRIRREVRHH 132

RESULT 31
CFAB_GORGO
ID CFAB_GORGO STANDARD; PRT; 764 AA.
AC Q864V9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Complement factor B precursor (EC 3.4.21.47) (C3/C5 convertase)
[Contains: Complement factor B Ba fragment; Complement factor B Bb
fragment].
DE GN Name=BF;
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Gorilla.
OX NCBI_TaxID=9595;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA Schneider P.M., Tantalaki E., Stradmann-Bellinghausen B., Rittner C.;
RA "Comparative analysis of human and primate complement C2 and factor B
RA genes.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor B which is part of the alternate pathway of the
CC complement system is cleaved by factor D into 2 fragments: Ba and
CC Bb. Bb, a serine protease, then combines with complement factor 3b
CC to generate the C3 or C5 convertase. It has also been implicated
CC in proliferation and differentiation of preactivated B
CC lymphocytes, rapid spreading of peripheral blood monocytes
CC stimulation of lymphocyte blastogenesis and lysis of erythrocytes.
CC Ba inhibits the proliferation of preactivated B lymphocytes (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: Cleavage of Arg-|-Ser bond in complement
CC component C3 alpha-chain to yield C3a and C3b, and Arg-|-Xaa bond
CC in complement component C5 alpha-chain to yield C5a and C5b.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the peptidase S1 family.
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC -!- SIMILARITY: Contains 3 Sushi (CCP/SCR) domains.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AY074664; AAM10005.1; -; Genomic DNA.
CC HSSP; P08174; 1H03.
CC SMR; Q864V9; 268-458, 476-764.
CC MEROPS; S01.196; -.
CC InterPro; IPR011360; Compl C2 B.
CC InterPro; IPR001254; Peptidase_S1_S6.
CC InterPro; IPR001314; Peptidase_S1A.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00084; Sushi; 3.
CC Pfam; PF00089; Trypsin; 1.
CC Pfam; PF00092; VWFA; 1.
CC PIRSF; PIRSF001154; Compl C2 B; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00453; VWFADOMAIN.
CC SMART; SM00032; CCP; 3.
CC SMART; SM00020; Tlyp_Spc; 1.
CC SMART; SM00327; VWFA; 1.
CC PROSITE; PS50923; SUSHI; 3.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC PROSITE; PS50234; VWFA; 1.
CC Complement alternate pathway; Glycoprotein; Hydrolase;
KW Immune response; Innate immunity; Plasma; Protease; Repeat;
KW Serine protease; Signal; Sushi; Zymogen.
FT SIGNAL 1 25 By similarity.
FT CHAIN 26 764 Complement factor B.
FT CHAIN 26 259 Complement factor B Ba fragment.
FT CHAIN 260 764 Complement factor B Bb fragment.
FT DOMAIN 35 100 Sushi 1.
FT DOMAIN 101 160 Sushi 2.
FT DOMAIN 163 220 Sushi 3.
FT DOMAIN 270 469 VWFA.
FT DOMAIN 477 757 Peptidase S1.

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FT ACT_SITE 526 Charge relay system (By similarity).
 FT ACT_SITE 576 Charge relay system (By similarity).
 FT ACT_SITE 699 Charge relay system (By similarity).
 FT CARBOHYD 122 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 142 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 285 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 378 N-linked (GlcNAc...) (Potential).
 FT DISULFID 37 By similarity.
 FT DISULFID 62 By similarity.
 FT DISULFID 103 By similarity.
 FT DISULFID 131 By similarity.
 FT DISULFID 165 By similarity.
 FT DISULFID 191 By similarity.
 SQ SEQUENCE 764 AA; 85526 MW; 2C6B9FFC2846D847 CRC64;

Query Match 33.3%; Score 55; DB 1; Length 764;
 Best Local Similarity 34.6%; Pred. No. 1e+02;
 Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 ETQHXKXGHLNSXERVWLKKLQD 29
 Db 733 QVPAHARDPHINLQVLPWLKELQD 758

RESULT 32

CFAB HUMAN STANDARD; PRT; 764 AA.
 AC P00751; O15006; Q29944; Q96HX6; Q9BTF5; Q9BX92;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Complement factor B precursor (EC 3.4.21.47) (C3/C5 convertase)
 DE (Properdin factor B) (Glycine-rich beta glycoprotein) (GBG) (PBF2)
 DE [Contains: Complement factor B Ba fragment; Complement factor B Bb fragment].
 DE Names=BF;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANTS ARG-28; GLN-28; GLN-32 AND SER-736.
 RX MEDLINE=91065702; PubMed=2249879; DOI=10.1007/BF00211644;
 RA Davrinche C., Abbal M., Clerc A.;
 RT "Molecular characterization of human complement factor B subtypes.";
 RL Immunogenetics 32:309-312(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANTS ARG-28 AND GLN-32.
 RC TISSUE=Liver;
 RX MEDLINE=94237735; PubMed=8181662; DOI=10.1016/0198-8859(94)90100-7;
 RA Mejia J.E., Jahn I., de la Salle H., Hauptmann G.;
 RT "Human factor B. Complete cDNA sequence of the BF*S allele.";
 RL Hum. Immunol. 39:49-53(1994).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANTS ARG-28 AND GLN-32.
 RC TISSUE=Liver;
 RX MEDLINE=94041399; PubMed=8225386;
 RA Schwaebig W., Luettig B., Sokolowski T., Estaller C., Weiss E.H., Meyer Zum Bueschenfelde K.-H., Whaley K., Dippold W.;
 RT "Human complement factor B: functional properties of a recombinant zymogen of the alternative activation pathway convertase.";
 RL Immunobiology 188:221-232(1993).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANTS ARG-28 AND GLN-32.
 RX MEDLINE=94067177; PubMed=8247029; DOI=10.1016/0161-5890(93)90450-P;
 RA Horuchi T., Kim S., Matsumoto M., Watanabe I., Fujita S., Volanakis J.E.;
 RT "Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic conversion by site-directed mutagenesis and expression.";
 RL Mol. Immunol. 30:1587-1592(1993).
 RN [5]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=14656967; DOI=10.1101/gr.1736803;
 RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S., Campbell R.D., Hood L.;
 RT "Analysis of the gene-dense major histocompatibility complex class III region and its comparison to mouse.";
 RL Genome Res. 13:2621-2636(2003).
 RN [6]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
 RA Jaatinen T., Kanerva J., Poutanen K.E., Saarinen-Pihkala U., Lokki M.-L.;
 RT "Expression and alternative splicing of human factor B gene in leukemic mononuclear cells.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA), AND VARIANTS HIS-9; GLN-32; TRP-32; SER-252; GUJ-565 AND GLU-651.
 RA Rieder M.J., Carrington D.P., Hastings N.C., Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
 RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-FHRC, Seattle, WA (URL: http://pga.gs.washington.edu)";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1), AND VARIANT TRP-32.
 RC TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP PROTEIN SEQUENCE OF 26-764, PARTIAL NUCLEOTIDE SEQUENCE, AND CARBOHYDRATES.
 RX MEDLINE=84161597; PubMed=6546754;
 RA Mole J.E., Anderson J.K., Davison E.A., Woods D.E.;
 RT "Complete primary structure for the zymogen of human complement factor B.";
 RL J. Biol. Chem. 259:3407-3412(1984).
 RN [10]
 RP PROTEIN SEQUENCE OF 260-764.
 RX MEDLINE=83204002; PubMed=6342610;
 RA Christie D.L., Gagnon J.;
 RT "Amino acid sequence of the Bb fragment from complement Factor B. Sequence of the major cyanogen bromide-cleavage peptide (CB-II) and completion of the sequence of the Bb fragment.";
 RL Biochem. J. 209:61-70(1983).
 RN [11]
 RP NUCLEOTIDE SEQUENCE OF 339-764.
 RX MEDLINE=83273641; PubMed=6308626;
 RA Campbell R.D., Porter R.R.;
 RT "Molecular cloning and characterization of the gene coding for human complement protein factor B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4464-4468(1983).
 RN [12]
 RP NUCLEOTIDE SEQUENCE OF 467-595 AND 752-764.
 RX MEDLINE=83039428; PubMed=6957884;

```
RA Woods D.E., Markham A.F., Ricker A.T., Goldberger G., Colten H.R.;  
RT "Isolation of cDNA clones for the human complement protein factor B, a  
RL class III major histocompatibility complex gene product.";  
RN Proc. Natl. Acad. Sci. U.S.A. 79:5661-5665(1982).  
RP NUCLEOTIDE SEQUENCE OF 16-259.  
RX MEDLINE=84158524; PubMed=6323161;  
RA Morley B.J., Campbell R.D.;  
RT "Internal homologs of the B $\alpha$  fragment from human complement  
RL component factor B, a class III MHC antigen.";  
RN EMO J. 3:153-157(1984).  
RP NUCLEOTIDE SEQUENCE OF 1-99.  
RC TISSUE=Blood;  
RX MEDLINE=87102880; PubMed=3643061; DOI=10.1016/0092-8674(87)90436-3;  
RA Wu L.C., Morley B.J., Campbell R.D.;  
RT "Cell-specific expression of the human complement protein factor B  
RL gene: evidence for the role of two distinct 5'-flanking elements.";  
RN Cell 48:331-342(1987).  
RP GLYCATION OF LYS-291.  
RX MEDLINE=91174758; PubMed=2006911;  
RA Niemann M.A., Bhown A.S., Miller E.J.;  
RT "The principal site of glycation of human complement factor B.";  
RL Biochem. J. 274:473-480(1991).  
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 467-764.  
RX MEDLINE=20105272; PubMed=10637221; DOI=10.1093/emboj/19.2.164;  
RA Jing H., Xu Y., Carson M., Moore D., Macon K.J., Volanakis J.E.,  
RN Narayana S.V.L.;  
RT "New structural motifs on the chymotrypsin fold and their potential  
RL roles in complement factor B.";  
RC EMBO J. 19:164-173(2000).  
CC -|- FUNCTION: Factor B which is part of the alternate pathway of the  
CC complement system is cleaved by factor D into 2 fragments: Ba and  
CC Bb. Bb, a serine protease, then combines with complement factor 3b  
CC to generate the C3 or C5 convertase. It has also been implicated  
CC in proliferation and differentiation of preactivated B  
CC lymphocytes, rapid spreading of peripheral blood monocytes,  
CC stimulation of lymphocyte blastogenesis and lysis of erythrocytes.  
CC Ba inhibits the proliferation of preactivated B lymphocytes.  
CC -|- CATALYTIC ACTIVITY: Cleavage of Arg-|-Ser bond in complement  
CC component C3 alpha-chain to yield C3a and C3b, and Arg-|-Xaa bond  
CC in complement component C5 alpha-chain to yield C5a and C5b.  
CC -|- SUBUNIT: Monomer.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=P00751-1; Sequences=Displayed;  
CC Name=2;  
CC IsoId=P00751-2; Sequences=VSP 005380, VSP 005381;  
CC -|- POLYMORPHISM: Two major variants, F and S, and 2 minor variants,  
CC as well as at least 14 very rare variants, have been identified.  
CC -|- SIMILARITY: Belongs to the peptidase S1 family.  
CC -|- SIMILARITY: Contains 1 peptidase S1 domain.  
CC -|- SIMILARITY: Contains 3 Sushi (CCP/SCR) domains.  
CC -|- SIMILARITY: Contains 1 VWFA domain.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; X72875; CAA51389.1; -; mRNA.  
CC EMBL; S67310; AAD13989.1; -; mRNA.  
CC EMBL; L15702; AAA16820.1; -; mRNA.  
CC EMBL; X00284; CAA25077.1; -; mRNA.  
CC EMBL; AF019413; AAB67977.1; -; Genomic_DNA.  
CC EMBL; AF349679; AAK30167.1; -; mRNA.  
CC EMBL; AF551849; AAN71991.1; -; Genomic_DNA.  
CC EMBL; BC004143; AAH04143.1; -; mRNA.  
CC  
CC EMBL; BC007990; AAH07990.1; -; mRNA.  
CC DR EMBL; K01566; AAA36225.2; -; mRNA.  
CC DR EMBL; J00125; -; NOT ANNOTATED CDS; Genomic_DNA.  
CC DR EMBL; J00126; AAA36226.1; -; mRNA.  
CC DR EMBL; J00185; AAA36219.1; ALT_SEQ; mRNA.  
CC DR EMBL; J00186; AAA36220.1; -; mRNA.  
CC DR EMBL; M15082; AAA59625.1; -; Genomic_DNA.  
CC  
CC Query Match 33.3%; Score 55; DB 1; Length 764;  
CC Best Local Similarity 34.6%; Pred.No.le+02;  
CC Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;  
CC  
CC QY 4 EIQXHNXGKHLNSXRVWLRKKLQD 29  
CC Db 733 QVPAHARDFHINLQVLPWLAKELQD 758  
CC  
CC RESULT 33  
CC CFAB_PANTR  
CC ID CFAB_PANTR STANDARD; PRT; 764 AA.  
CC AC Q864W0;  
CC DT 29-MAR-2004 (Rel. 43, Created)  
CC DT 29-MAR-2004 (Rel. 43, Last sequence update)  
CC DT 13-SEP-2005 (Rel. 48, Last annotation update)  
CC DE Complement factor B precursor (EC 3.4.21.47) (C3/C5 convertase)  
CC DE [Contains: Complement factor B Ba fragment; Complement factor B Bb  
CC fragment].  
CC GN Name=BF;  
CC OS Pan troglodytes (Chimpanzee).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
CC OC Pan.  
CC OX NCBI_TaxID=9598;  
CC [1]  
CC RP NUCLEOTIDE SEQUENCE.  
CC RC TISSUE=Blood;  
CC RA Schneider P.M., Tantalaki E., Stradmann-Bellinghausen B., Rittner C.;  
CC RT "Comparative analysis of human and primate complement C2 and factor B  
CC genes.";  
CC RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
CC CC -|- FUNCTION: Factor B which is part of the alternate pathway of the  
CC complement system is cleaved by factor D into 2 fragments: Ba and  
CC Bb. Bb, a serine protease, then combines with complement factor 3b  
CC to generate the C3 or C5 convertase. It has also been implicated  
CC in proliferation and differentiation of preactivated B  
CC lymphocytes, rapid spreading of peripheral blood monocytes,  
CC stimulation of lymphocyte blastogenesis and lysis of erythrocytes.  
CC Ba inhibits the proliferation of preactivated B lymphocytes (Bb  
CC similarity).  
CC -|- CATALYTIC ACTIVITY: Cleavage of Arg-|-Ser bond in complement  
CC component C3 alpha-chain to yield C3a and C3b, and Arg-|-Xaa bond  
CC in complement component C5 alpha-chain to yield C5a and C5b.  
CC -|- SUBUNIT: Monomer (By similarity).  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- SIMILARITY: Belongs to the peptidase S1 family.  
CC -|- SIMILARITY: Contains 1 peptidase S1 domain.  
CC -|- SIMILARITY: Contains 3 Sushi (CCP/SCR) domains.  
CC -|- SIMILARITY: Contains 1 VWFA domain.  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; AY074663; AAM10004.1; -; Genomic_DNA.  
CC DR HSSP; P08174; 1H03.  
CC DR SMR; Q864W0; 268-458, 476-764.  
CC DR MEROPS; S01.196; -.  
CC DR InterPro; IPR011360; Compl_C2_B.  
CC DR InterPro; IPR001254; Peptidase_S1_S6.  
CC DR InterPro; IPR001314; Peptidase_S1A.  
CC DR InterPro; IPR000436; Sushi_SCR_CCP.
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DR InterPro: IPR002035; VWF_A.
DR Pfam: PF00084; Sushi; 3.
DR Pfam: PF00089; Trypsin; 1.
DR Pfam: PF00092; VWF; 1.
DR PIRSF: PIRSF001154; Compl C2 B; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00453; VWFADOMAIN.
DR PROSITE: PS00923; SUSHI; 3.
DR PROSITE: PS00240; TRYPSIN DOM; 1.
DR PROSITE: PS00134; TRYPSIN HIS; 1.
DR PROSITE: PS00135; TRYPSIN SER; 1.
DR PROSITE: PS00234; VWF; 1.
KW Complement alternate pathway: Glycoprotein; Hydrolase;
KW Immune response; Innate immunity; Plasma; Protease; Repeat;
KW Serine protease; Signal; Sushi; Zymogen.
FT SIGNAL 1 25 By similarity.
FT CHAIN 26 764 Complement factor B.
FT CHAIN 26 259 Complement factor B Ba fragment.
FT CHAIN 260 764 Complement factor B Bb fragment.
FT DOMAIN 35 100 Sushi 1.
FT DOMAIN 101 160 Sushi 2.
FT DOMAIN 163 220 Sushi 3.
FT DOMAIN 270 469 VWFA.
FT DOMAIN 477 757 Peptidase S1.
FT ACT_SITE 526 526 Charge relay system (By similarity).
FT ACT_SITE 576 576 Charge relay system (By similarity).
FT ACT_SITE 699 699 Charge relay system (By similarity).
FT CARBOHYD 122 122 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 142 142 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 285 285 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 378 378 N-linked (GlcNAc..) (Potential).
FT DISULFID 37 76 By similarity.
FT DISULFID 62 98 By similarity.
FT DISULFID 103 145 By similarity.
FT DISULFID 131 158 By similarity.
FT DISULFID 165 205 By similarity.
FT DISULFID 191 218 By similarity.
SQ SEQUENCE 764 AA; 85513 MW; 972C097B0934FED1 CRC64;

Query Match 33.3%; Score 55; DB 1; Length 764;
Best Local Similarity 34.6%; Pred. No. 1e+02;
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 EIQHNKXGHLNSKXRVLEWLKKLQD 29
Db 733 QVPAHARDFHINLFQVLPLWKKLQD 758

RESULT 34
CFAB_PONPY STANDARD; PRT; 764 AA.
AC Q864W1;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Complement factor B precursor (EC 3.4.21.47) (C3/C5 convertase)
DE [Contains: Complement factor B Ba fragment; Complement factor B Bb fragment].
DE Name=BF;
GN Pongo pygmaeus (Orangutan).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RS Schneider P.M., Tantalaki E., Stradmann-Bellinghausen B., Rittner C.;
RT "Comparative analysis of human and primate complement C2 and factor B genes.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor B which is part of the alternate pathway of the complement system is cleaved by factor D into 2 fragments: Ba and Bb. Bb, a serine protease, then combines with complement factor 3b

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Query Match

33.3%; Score 55; DB 1; Length 764;

```
Best Local Similarity 34.6%; Pred. No. 1e+02;
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 EIQXNKGKHLNSXERVWLKQLQD 29
Db 733 QVPAHARDPHINLFQVLPWLKQLQD 758

RESULT 35
Q53F89 HUMAN
ID Q53F89_HUMAN PRELIMINARY; PRT; 764 AA.
AC Q53F89;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Complement factor B preproprotein variant (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA Matuyama K.; Sugano S.;
RT "Oligo-capping : a simple method to replace the cap structure of
eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
[2]
RN [2]
RP NUCLEOTIDE SEQUENCE
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
[3]
RN [3]
RP NUCLEOTIDE SEQUENCE
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
EMBL; AK234007; BAD97120.1; -; mRNA.
DR GO: 0005576; C:extracellular region; IEA.
DR GO: 0004263; F:chymotrypsin activity; IEA.
DR GO: 0004295; F:trypsin activity; IEA.
DR GO: 0006956; P:complement activation; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR Sush.
FW NON_TER 1 1
SQ SEQUENCE 764 AA; 85562 MW; 7574383E5FF7CC95 CRC64;

Query Match 33.3%; Score 55; DB 2; Length 764;
Best Local Similarity 34.6%; Pred. No. 1e+02;
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 EIQXNKGKHLNSXERVWLKQLQD 29
Db 733 QVPAHARDPHINLFQVLPWLKQLQD 758

RESULT 36
Q53F67 HUMAN
ID Q53F67_HUMAN PRELIMINARY; PRT; 764 AA.
AC Q53F67;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE B-factor, properdin.
GN Name=BF; ORFNames=DAQB-331112.9-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA Brown J.;
```

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Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
EMBL; AL844853; CAI41860.1; -; Genomic_DNA.
SNR; Q5JP67; 268-458, 476-764.
DR GO: 0005576; C:extracellular region; IEA.
DR GO: 0004263; F:chymotrypsin activity; IEA.
DR GO: 0004295; F:trypsin activity; IEA.
DR GO: 0006956; P:complement activation; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR011360; Compl_C2_B.
DR InterPro; IPR011254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sush. SCR_CCP.
DR Pfam; PF00084; Sush. 3.
DR Pfam; PF00089; Trypsin; 1.
DR Pfam; PF00092; VWFA; 1.
DR PIRSF; PIRSF001154; Compl_C2_B; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00032; CCP; 3.
DR SMART; SM00020; Tryp_Spc; 1.
DR SMART; SM00327; VWFA_1.
DR PROSITE; PS0923; SUSHI; 3.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PROSITE; PS0234; VWFA; 1.
KW Hydrolase; Protease; Serine protease; Sush.
SQ SEQUENCE 764 AA; 85534 MW; 40A77DA6D77CCFB3 CRC64;

Query Match 33.3%; Score 55; DB 2; Length 764;
Best Local Similarity 34.6%; Pred. No. 1e+02;
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 EIQXNKGKHLNSXERVWLKQLQD 29
Db 733 QVPAHARDPHINLFQVLPWLKQLQD 758

RESULT 37
Q5ST50 HUMAN
ID Q5ST50_HUMAN PRELIMINARY; PRT; 764 AA.
AC Q5ST50;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE B-factor, properdin.
GN Name=BF; ORFNames=XXBac-BCX11619.3-001; XXBac-BPG116M5.11-001;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP NUCLEOTIDE SEQUENCE
RA Griffiths C.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL662849; CAI17456.1; -; Genomic_DNA.
DR EMBL; AL645922; CAI41726.1; -; Genomic_DNA.
DR SNR; Q5ST50; 268-458, 476-764.
DR GO: 0005576; C:extracellular region; IEA.
DR GO: 0004263; F:chymotrypsin activity; IEA.
DR GO: 0004295; F:trypsin activity; IEA.
DR GO: 0006956; P:complement activation; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR011360; Compl_C2_B.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
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DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF00084; Sushi; 3.
 DR Pfam; PF00089; Trypsin; 1.
 DR Pfam; PF00092; VWA; 1.
 DR PIRSF; PIRSF001154; Compl C2 B; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00032; CCP; 3.
 DR SMART; SM00020; Tryp SPC; 1.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00923; SUSHI; 3.
 DR PROSITE; PS02440; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR PROSITE; PS0234; VWFA; 1.
 DR Hydrolase; Protease; Serine protease; Sushi.
 KW HYDROLASE; PROTEASE; SERINE PROTEASE; SUSHI.
 SQ SEQUENCE 764 AA; 85533 MW; 8BB6C10CC6AC200 CRC64;

Query Match 33.3%; Score 55; DB 2; Length 764;
 Best Local Similarity 34.6%; Pred. No. 1e+02;
 Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 EIQXHXGHLNSXERVELRKLQD 29
 DB 733 QVPAHARDPHINLQVLPWLKELQD 758

RESULT 38
 Q83JQ3 SHIFL
 ID Q83JQ3 SHIFL PRELIMINARY; PRT; 118 AA.
 AC Q83JQ3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE IS629 ORF2.
 GN OrderedLocusNames=SF2978;
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=301 / Serotype 2a;
 RX MEDLINE=2272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 Yu J.;
 RA "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 DR EMBL; AE003674; AAN44459.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 118 AA; 13701 MW; D81C780B9EBE303B CRC64;

Query Match 32.7%; Score 54; DB 2; Length 118;
 Best Local Similarity 33.3%; Pred. No. 20;
 Matches 9; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 6 QXHXGHLNSXERVELRKLQDVHN 32
 DB 34 QRHFDKSSRAQRDNLKKEIQRYVD 60

RESULT 39
 Q7R8J7 PLAYO
 ID Q7R8J7 PLAYO PRELIMINARY; PRT; 323 AA.
 AC Q7R8J7;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein.
 GN Name=PY07225;
 OS Plasmodium yoelii yoelii
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=2255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
 Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V.,
 Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL01002601; EAA19607.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 323 AA; 38968 MW; 4BB74EF385743973 CRC64;
 Query Match 32.7%; Score 54; DB 2; Length 323;
 Best Local Similarity 34.6%; Pred. No. 57;
 Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 QY 8 HNXGHLNSXERVELRKLQDVHNY 33
 DB 296 HEWKRLRYNEKFYIKKPKSIHNV 321

RESULT 40
 Q5ZIS6 CHICK
 ID Q5ZIS6_CHICK PRELIMINARY; PRT; 1252 AA.
 AC Q5ZIS6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORNames=RCMB04_2307;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CB; TISSUE=Bursa;
 RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
 RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
 RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
 RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
 RT gene function analysis";
 RL Genome Biol. 6:R6-R6(2005).
 DR EMBL; AJ720708; CAG32367.1; -; mRNA.
 DR GO; GO:000785; C:nucleus; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003682; F:chromatin binding; IEA.
 DR GO; GO:0006333; F:chromatin assembly or disassembly; IEA.
 DR InterPro; IPR001606; ARID.
 DR InterPro; IPR000953; Chromo.
 DR InterPro; IPR002399; Tudor.
 DR Pfam; PF01388; ARID; 1.
 DR SMART; SM00501; BRIGT; 1.
 DR SMART; SM00298; CHROMO; 1.
 DR SMART; SM00333; TUDOR; 1.

DR PROSITE; PSS1011; ARID; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1252 AA; 141790 MW; B9FA32177E73B96E CRC64;
 Query Match 32.7%; Score 54; DB 2; Length 1252;
 Best Local Similarity 38.1%; Pred. No. 2.3e+02;
 Matches 8; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
 QY 13 HLNSEXRVWLRKKLQDVHNY 33
 Db 1174 NMSSTERISFLOEKLOEIRKY 1194

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